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(57) Abstract

This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.

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ANNEX TO THE STERNATIONAL SEARCH REPORT ON INTERNATIONAL SPATENT APPLICATION NO.

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HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE NARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

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There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is Moreover, techniques for a very small part of the total (5% or less). On the other hand, even generating cDNAs are also well known. supposing near perfect recovery of cDNAs corresponding to all expressed mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of Nonetheless, the cDNA approach at least substantially reduces inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

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other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambig: :sly classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. identified in this way were further characterised and found to be useful in a variety of standard applic ions, including physical mapping. Unfortunately, such a process is insufficient. the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than This difficulty is exacerbated by the wide range of once increases. abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

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Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

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Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

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- (a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
- 30 (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
- (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
 - (d) carrying out an extension synthesis in the mixture produced in step (c).

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Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

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Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually, therefore, all DNA species will be present at the same concentration.

The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirely, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

- In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid population is treated by:
 - (a) subjecting the nucleic acid to the action of a reagent,

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preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

- (b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adaptored cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and
- (c) selecting and separating only those adaptored cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok 1.

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An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin

reaction in selecting and separating desired adaptored molecules.

Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adaptored molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

40 Preferably the adaptors are short duble-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

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and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adaptored end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adaptoring" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

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- (a) -a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- 15 (c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids -Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 pl390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p^{a} 1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, pl23 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

The present invention also envisages DNA constructs comprising 40 fragments or sequences as referred to above with a control or regulatory sequence.

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The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal

Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology: Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

antibodies using standard techniques.

D. M. et al., pl08 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic Bacillus subtilis, eurkaryotic yeast, mammalian cows milk vectors, and other methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

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It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

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used as a means for determining the existence of new members of existing gene far lies, new human genes when previously only non-human and new genes when previously no genes were known genes were know (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding and hence enables the manufacture of genes and their products, molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may For example, new receptors or receptor already be apparant. agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 pl (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltfuz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Procaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher

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eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. Gene 40 p183 1985), Shimuzu, Y et al., Gene 65, p141 (1988), Straus, D. and Gilbert, W. Proc. Natl. Acad. Sci. 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. Nature 353 pp605-607 (1991), Rudensky, A., Y., et al., Nature 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated It is desirable, from a sequence or fragment of this invention. although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodi s. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide. Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., C. Methods Enzmol. 153 p461-481 (1987). Another alternative is rais monoclonal antibodies against the purified protein.

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The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg For example tumour markers may be found and used to target The antibodies can also be used to detect or therapeutic agents. monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

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Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

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clone.

This invention will now be further described and illustrated by means of the following Examples.

All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age foetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA (mRNA) was isolated from 200 to 400 μg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 μ g of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's · 5

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instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

The column eluate was adjusted to 10 mM $\rm Mg^{2+}$ and then the purified cDNA was restricted by the action of 1 unit per 10 μl of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

The adaptors used were oligonucleotides 5' N4N4N4TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTCGCAGGAGAAGGA (SEQ ID: 1195) and 5' AAN4N4TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' $\mathtt{TTN_4N_4TCTCGGACAGTGCTCCGAGAAC}$ (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added MgCl $_2$ to 10mM, ATP to 10mM and 0.025 units/ μ l of **T4** DNA ligase. The oligonucleotide biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90 μ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

The column eluate was adjusted to 25mM Mg2+, 0.5mM dNTPs in a final volume of 200 μ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 μl of streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary the 5'

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GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

Un-biotinylated cDNAs were washed from the beads with $400\mu l$ each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg²⁺. The beads were then resuspended in 240 μl of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60 μl .

Four of the 60 μ l aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adaptored fragments. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAA (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 μ l of resuspended beads were added to each reaction to remove the biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

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of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8 μ l or 12.5 % whichever was the larger but not exceeding 12 μ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg²⁺, 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40 μ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60 μ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. Different cohesive ends were (Nucl. Acids Res. 18, p6156 (1990)). produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. 75 μ l or 75 % of the column eluate, whichever was least, were added 9.5 μ l of 100mM TrisHCl pH7.4, 100 mM MgCl2, and 9.5 μ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in The enzyme was removed by a water bath at 37°C for 30 minutes. extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

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and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptoring the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' 5 GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptoring were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and 10 HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 ligations standard controls for the Suitable transformations were also included. 15

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing $50\mu g/ml$ ampicillin and $10\mu g/ml$ tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing $100\mu l$ of L-broth and $50\mu g/ml$ ampicillin. Growth was allowed to occur for 16 hours at 37° C. $100\mu l$ of 50% or 30% glycerol was added to plates which were archived at -20° C or -80° C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing $50\mu g/ml$ of ampicillin, prepared at the same time as they had been grown archive. plating out from the in liquid culture, or after Alternatively, fresh liquid cultures were inoculated from the archive. In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAAACGACGGCCAGT

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(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in $40\mu l$ reactions containing 2.5mM Mg²⁺, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to steptravidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic workstation attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluoroscein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" In both cases, files of called bases were entered into a Sybase[™] database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

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A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTCGACAAGCTTGAATTCGCGGCCGC(T) $_{26}$, (SEQ ID: 1210) was used at 1 μ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100 μ l with water.

PCRs were then performed in reactions containing 1 μ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin, 200 μ M dNTPs, 10 uci a³²P dCTP, 1 μ M each of the primers 11ADl, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°c for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

40 Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

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cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into Eccoli Y1090 and plated out for colour selection of recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyocarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

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Clear plaques from each library were resuspended in 5 μ l of Tris-HCl pH 8, 1 mM EDTA. 2 μ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that the oligonucleotides used as primers for the lambda gtll clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

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Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

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Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID

Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

. (1) GENERAL INFORMATION

(i)	AP	PL	IC	AN	T
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- (A) NAME: MEDICAL RESEARCH COUNCIL
- 5 (B) STREET: 20 PARK CRESCENT
 - (C) CITY: LONDON
 - (E) COUNTRY: ENGLAND
 - (F) POSTAL CODE: WIN 4AL
- 10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES
 - (iii) NUMBER OF SEQUENCES: 1213
 - (iv) COMPUTER READABLE FORM:

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- (A) MEDIUM TYPE: DISKETTE
- (B) COMPUTER: IBM PC COMPATIBLE
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: EXTRACT

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(2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID :1:

	GCCGATTCGT	GACCAAGAAG	GCTCTGTGCA	TTCGGGTTTT	CCAGGAGACT	50
35	CAAAAGCTGA	AGAAGCGAAG	AAGAGCCTTA	AAGGCTGCAG	CAGCAGCTCA	100
	ATAAACAAGC	AAAGCGGAGG	AACCCAGACA	GCCCTTGTCC	AAAGCCATAC	150
40	CAATATGATC	TATCTTCTAA	TGTATCCATG	TTGTAATTAT	ATATGTGTCT	200
40	GTGTGTGTCG	AAATCTCTAG	ACATACAGAT	ATATATTCAT	ATATCATATA	250

	TATATATATA CACA	264
	(2) INFORMATION FOR SEQ ID :2:	
5	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 124 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :2:	
15	AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT	50
	GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC	100
20	CTGGGGAGGG GGTCATTGTT CTCT	124
20	(2) INFORMATION FOR SEQ ID :3:	
•	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 333 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :3:	
	ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC	50
35	TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC	100
	TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC	150
40	AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA	200
	GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA	250

	ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG	300
	TCACATATTA GGAACTGATA ACATAAGGTA AAC	333
5	(2) INFORMATION FOR SEQ ID :4:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 200 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :4:	•
	AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC	50
	GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTTCT GTCTTTATGT	100
20	AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAAA CAGGAATTTC	150
	TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCCC CTGCCCCCAT	200
25	(2) INFORMATION FOR SEQ ID :5:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 213 base pairs	•
	(B) TYPE: nucleic acid	•
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :5:	
	ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA	50
	AGATTTGCCA AATTGTAGCC TACTGGATTC CGGTTCTCTT GACATCTCTT	100
40	TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA	150

.•	ATTAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA	200
	GCACAATCAC TAG	213
5	(2) INFORMATION FOR SEQ ID :6:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 345 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
1:5	(xi) SEQUENCE DESCRIPTION: SEQ ID :6:	
	CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG	50
	GAAGTTTTAA GCTAAGATTT GCCAAATTGT AGCCTACTGG ATTCCGGTTC	100
20	TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC	150
	GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG	200
25	AAAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA	250
	TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT	300
30	GTGGCCCATA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC	345
	(2) INFORMATION FOR SEQ ID :7:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 159 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

. •	TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG	50
	GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA	100
5 .	GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT	150
	TTCTTTTCC	159
	(2) INFORMATION FOR SEQ ID :8:	
10	The state of the s	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs	
	(B) TYPE: nucleic acid	٠
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :8:	٠
20	(XI) BEGENES ELECTION COL CO.	
	ATATTTCAAT CGAACAAAAA GGAAACTTTT TTTGAACTTA TTGAGGCTCT	50
	ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCCT	100
25	TGCCTGGCTG GGGGTTTGAT TCGC	124
	(2) INFORMATION FOR SEQ ID :9:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 259 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :9:	•
	CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA	50
40		
	TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG	100

	ACCGGGATGC AGTGTCAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG	150
	GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCCTGTTC	200
5	CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA	250
	GAAAATAGA	259
	(2) INFORMATION FOR SEQ ID :10:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 216 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :10:	·
20	GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCCAGGG CCCTCAAGAA	50
	GCTCCTGCAC ACAATAAACG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT	100
25	CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA	150
	GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA	200
30	CTGTGACAAG GGGCCC	216
30	(2) INFORMATION FOR SEQ ID :11:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 205 base pairs	
3 5	(B) TYPE: nucleic acid	•
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :11:

	CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG	50
	CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA	100
5	AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT	150
	GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG	200
	GGATG	205
10	(2) INFORMATION FOR SEQ ID :12:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 267 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :12:	
	TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC	50
25	AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT	100
	CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA	150
	GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG	200
30	TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA	250
	TATGCCATTC TCGGTGA	267
35	(2) INFORMATION FOR SEQ ID :13:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 116 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOCY: linear	

• •	(xi) SEQUENCE DESCRIPTION: SEQ ID :13:	
	GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG	50
· 5	GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG	100
,	CAATGTGAAG CTGAAC	116
10	(2) INFORMATION FOR SEQ ID :14:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 296 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :14:	
	TTCGAACTTA CCAGCATCAT GTTTGGTCTC TTCGTATGGT CAAACTTCAA	50
25	CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG	100
25	CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT	150
	ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACATCTA	200
30	AGGGGTGCAA GGACCAGGCT TTGATTTCAA ATTATAATCT AATGCTCACT	250
	CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA	296
35	(2) INFORMATION FOR SEQ ID :15:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 123 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :15:	
	CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG	50
5	AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC	100
	CAAACTCGAT TCAAAGAGCA ATA	. 123
	(2) INFORMATION FOR SEQ ID :16:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 262 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
-		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :16:	
20	CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT	50
	GGCATTGTCA GAAAAATTTA ACAGGTTTAT TTATAATTAT CATAAAGTTG	100
25	ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG	150
	TCTCCGCATT TATATTAAAA ATTCACACAC AAATGAAATG	200
20	CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA	250
30	CTTTTGACTC TA	262
	(2) INFORMATION FOR SEQ ID :17:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 169 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :17:	
	TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG	50
5	AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT	100
	TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATTT	150
10	TCAAGAAACG TGCATCAGC	169
10	(2) INFORMATION FOR SEQ ID :18:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 221 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :18:	
	AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCCATA GAAATGGCCA	50
25	AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA	100
	CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA	150
30	TTATTAAAAT ACTGGCTTCG GTTTCTTTTT TTCCTTTGCA AAGTTTCCTA	200
	CATATATGTC TTTTACAGTA T	221
	(2) INFORMATION FOR SEQ ID :19:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 135 base pairs(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40		

.•	(xi) SEQUENCE DESCRIPTION: SEQ ID :19:	
	TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA	50
5	TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT	100
	TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC	135
	(2) INFORMATION FOR SEQ ID :20:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 314 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :20:	
20	(XI) SEQUENCE DESCRIPTION: SEQ ID :20:	
	GTTATCTATC TATCTTGCAG TTTACCTATC TGATCTGATC	50
	TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA	100
25	AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG	150
	TTATTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT	200
		200
	TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTAA AAAAAATTGT	250
30		
	ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG	300
	##N##N##N# N##CN	214
	TTATTAGTAA ATGA	314
35	(2) INFORMATION FOR SEQ ID :21:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

-	(xi) SEQUENCE DESCRIPTION: SEQ ID :21:	
5	TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT	50
	TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC	100
	TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT	150
10	TCCTCTTTCA ATATTTCTGT TTCTTGCC	178
	(2) INFORMATION FOR SEQ ID :22:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 188 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :22:	
	ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT	50
25	ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA	100
	GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT	150
30	TTTCTTAAAA CAACACTT ATTATCTTAC AAATCTGT	188
	(2) INFORMATION FOR SEQ ID :23:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 152 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

. •	(xi) SEQUENCE DESCRIPTION: SEQ 1D :23:	
	TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTTATA TTTTTNAAAT	50
5	GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTTAAATT CTCCAATTTT	100
	TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA	150
	GG	152
10	(2) INFORMATION FOR SEQ ID :24:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 83 base pairs	
15	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :24:	
	ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA	. 50
25	ACTITIGCAC ACTITITCAA CGGTCCCACC ACA	83
25	ROTTIGORO ROTTITION. CONTROLLE SANTO	·
	(2) INFORMATION FOR SEQ ID :25:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 176 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :25:	
	AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA	. 50
40	ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT	100

	ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC	150
	CTACATCTGG CTGACATTTA CATTTT	17.6
5	(2) INFORMATION FOR SEQ ID :26:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 232 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :26:	
	AAATGTATGA TCAGAAAATA GGTACGCTTT TAAAATATTT GAACAGAAAA	50
	GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC	100
20	TTTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT	150
	TTAAGTACTG ACGAAGAAGA CTAAAACAAT CATTTTTAA CAATATTTAA	200
25	AAGGATCATA TAGTCGACTT TTAAAACANC CC	232
	(2) INFORMATION FOR SEQ ID :27:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :27:	
	GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG	50
40	GCCCAATCTT CCCAAGTCCA CACAGGAGGG AAACATTGTT TGCGTAAATA	100

	CGCAATGCAA AATTTNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTCG	150
	AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC	192
. 2	(2) INFORMATION FOR SEQ ID :28:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 201 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :28:	
	TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT	50
	TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT	100
20	GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT	150
	CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT	200
25	Ť	201
	(2) INFORMATION FOR SEQ ID :29:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 275 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		~
	(xi) SEQUENCE DESCRIPTION: SEQ ID :29:	
	AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTCAC TTTATTGGCC	50
40		100

••	ATTTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT	150
	AACTATTTTA ATTACATATA ATGTAACTAA TGGAGAGATT TATAGAGAAT	200
5	TTTGTTTTTT TGTCATATAC TCCATTTCGA AGACAGATAT GATAGAACTA	250
	GARATTARGT TGCATTTCTG CAAGT	275
	(2) INFORMATION FOR SEQ ID :30:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 122 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
_		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :30:	
20	GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC	50
	ATTCATCAAC AAGATTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC	100
25	TGATCACAAC AACCGTCTTT GA	122
	(2) INFORMATION FOR SEQ ID :31:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 197 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :31:	
	GGATTTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT	50
40		100

	. AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC	150
	TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC	197
. 5	(2) INFORMATION FOR SEQ ID :32:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 97 base pairs	
10	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :32:	
	ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG	50
20	TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC	97
	(2) INFORMATION FOR SEQ ID :33:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs	
25	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :33:	
	CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA	50
35	CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT	100
	AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC	150
40	AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC	200
	CTAGGAAAAA ATAAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT	250

	 CACAATAAGA	260
	(2) INFORMATION FOR SEQ ID :34:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :34:	
15	GGACNTGCGC NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG	50
	ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT	100
20	GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNNGAT AAGGTGTGGA	150
20	NTTNGGTTAA AGACAAGG	168
	(2) INFORMATION FOR SEQ ID :35:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 173 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :35:	
35	CTCGNACACT GTGGAGAGCC TGCGNNNNNN NNGGTNTACT CAGGGGGACG	50
	AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT	100
40	GCTNNNGTGG TCCCTTAGNA 3CCGAGNAGG TGGGCGCGAG GTGAANAAGG	150
40	TGCNNGTGCG AGAGTGCGTG ATT	173

	 (2) INFORMATION FOR SEQ ID :36:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 134 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :36:	
	AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA	50
15	CAACTAATAA TGATTTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA	100
	GTTTTGCTAA CCTTGGTAAG CTTGTTTACC GTTT	134
20	(2) INFORMATION FOR SEQ ID :37:(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 160 base pairs	
25	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :37: TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA	5(
	ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTTGCTC AGTACAGACN	100
35	GATTTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC	150
	ATGACTTCTT	160
40	(2) INFORMATION FOR SEQ ID :38: (i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 140 base pairs

.•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
[•] 5	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :38:	•
	TO THE PROPERTY OF THE PROPERTY AND THE PROPERTY OF THE PROPER	50
	CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAATCCCA CCCTCACACG	
10	ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT	100
	ATTITITACC TICNITACTI NGCCCTICNI INCCCI	
	CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC	140
15	(2) INFORMATION FOR SEQ ID :39:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 203 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	The same and the s	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :39:	
	AGCAAGTATC ANNNNNNNN ATACATTTGA ATTCAAGTTG TTTTTTGTCA	50
	AGCAAGIAIC ANNININININ AIRCAITION COLLEGE DOCUMENTO	
	AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG	100
30		
	GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG	150
	CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGGA	200
35	AAA	203
	•	
	(2) INFORMATION FOR SEQ ID :40:	
	A CONTRACT OF THE CONTRACT OF	
	(i) SEQUENCE CHARACTERISTICS	
40	(A) LENGTH: 170 base pairs(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(C) SIVUADEDIAESS. GOGDIC	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :40:	
	GAAAAGCNNN NNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG	50
10	ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA	100
10	ACTAATGAGA AGATGTTCAC CTCTCTCTG AAAACTATGC CCACCAGACC	150
	GTTTAGCCTC TGCTCAAGCT	170
15	(2) INFORMATION FOR SEQ ID :41:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :41:	
	GCTGCATGTT TCCTTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA	50
30	AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT	100
	ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA	150
	CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA	200
35	ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG	250
	AAATTTGATT TGTAATAAAA	270
40	(2) INFORMATION FOR SEQ ID :42:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: doddie	
	(D) TOPOLOGY: linear	
. 2		
	A CONTRACT PROGRAMME CONTRACTOR AND	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :42:	
	AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC	50
10	AGAGOTGCAT GITTCOTTGA TITGAAGOTT GAAGITGAGA. GOTOTTAAG	
10	CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT	100
	AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC	150
15	ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT	200
	GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA	245
	(2) INFORMATION FOR SEQ ID :43:	
20	A CONTRACT OF THE CONTRACT OF	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :43:	
30	. •	
	TACACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC	50
	TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA	100
	A TO A SOLO A TOTAL OF THE MOSES	. 124
35	ATGAAGACAC TTTACACTTT TCGG	124
•	(2) INFORMATION FOR SEQ ID :44:	
	(2) Intommitton for one of the train	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 144 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

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43

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :44:	
	GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG	50
10	GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA	100
10	AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA	144
	(2) INFORMATION FOR SEQ ID :45:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 177 base pairs(B) TYPE: nucleic acid	•
20	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :45:	
25	ACTGATTCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT	50
	CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA	100
30	CAAAAAAAA AACAACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA	150
	GAAATTTAAT GTTTTTCATA ACATGAA	177
	(2) INFORMATION FOR SEQ ID :46:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

40

••	(xi) SEQUENCE DESCRIPTION: SEQ ID :46:	•
	ACTGATTCTG CGAAAATACC CCCTTTTTAT TAGTGGCATG CTCATTCACT	50
5	TTATCTTTAT ATTCAAATAA GTTATTTCGC TTTCACTGTT TTAACAAAAA	100
	AAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT	150
	TAATTCACAC GGAAAAACCA AGACAATTTC ACAACTTCTG GACACAACCA	200
10	TCAACACAGG ACATTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT	250
	CCCAGA	256
15	(2) INFORMATION FOR SEQ ID :47:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 155 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :47:	
	GAGAAAAGTC NNNNNNNNA GGTTAATCTA ACTTTTCTTG CTTATTTCAG	50
	CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTT	100
30	AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG	150
	AGCAA	155
35	(2) INFORMATION FOR SEQ ID :48:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 68 base pairs(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	•

•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :48:	
	GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAAATGAT GAATAAGATA	50
5	TTTNNACAAA GATACACG	68
	(2) INFORMATION FOR SEQ ID :49:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 244 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :49:	
20	CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG	50
	GGCCTAGCTA AATTTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA	100
	ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC	150
25		200
	TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG	200
•	AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG	244
30	(2) INFORMATION FOR SEQ ID :50:	
•		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 81 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :50:	

ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA

	·	
	GGANAAAGNG CCGCCCTACG TGGTACACAC A	81
	(2) INFORMATION FOR SEQ ID :51:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :51:	
15	GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA	50
	AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT	100
20	TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT	150
20	TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT	200
	TTATACCAGA AGNATGACCA CTG	223
25	(2) INFORMATION FOR SEQ ID :52:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 49 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :52:	
	TATGGTTTNT TGTAAAAAG CTCANNNANA AAGGGANNGG CTTAAGAGA	49
	(2) INFORMATION FOR SEQ ID :53:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 213 base pairs	
	(11) 2211-11-	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: GOUDTE	
	(D) TOPOLOGY: linear	
· 5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :53:	
	(A1) Bagodhoa babonararon dag ib voor	•
10	CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
10	TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
	TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
15	TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA	200
	TTCAATAATC AAA	213
	(2) INFORMATION FOR SEQ ID :54:	
20		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 166 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :54:	
30	GCGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTTGTGTG	. 50
	CGTNNTTGCG TANGGGGNGG GTTTNGGCAG GTGTTGCCGG TAGCNAAACN	100
35	GTTGGCCCCA TNGCCNGNAT TGNNNCCCCN CNNGGGAANG GGGGGGGNGA	150
	CCNNAGNGGG AAAAAA	166
10	(2) INFORMATION FOR SEQ ID :55:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 75 base pairs	
	(,	

• •	(B) TIPE: nucleic acid	
	(C) STRANDEDNESS: doubl	
	(D) TOPOLOGY: linear	
5	·	
_		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :55:	
	• • •	
	ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT	50
10		
	NGNCGTTGTN GCTGCCAAGC GACAT	75
		•
	(2) INFORMATION FOR SEQ ID :56:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 181 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :56:	
25	AATNNNNCC TATTTTGTAA TTTTTTTGAA AAAAGTTCAA TGTTCAGTTT	50
	TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA	100
		150
	AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA	150
30	·	101
	TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A	181
	(2) INFORMATION FOR SEQ ID :57:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 130 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	·	

	••	(xi) SEQUENCE DESCRIPTION: SEQ ID :57:	
		TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA	50
· 5		GATGACGNNA TCCAATTTCA GAACACCACA GGGCACTGGC ACACAGAGGG	100
		GATTATTACA GAACCACTGA GATGACATTT	130
	٠	(2) INFORMATION FOR SEQ ID :58:	
10		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 157 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
15		(D) TOPOLOGY: linear	
12		(b) for obodi. If hear	
			•
		(xi) SEQUENCE DESCRIPTION: SEQ ID :58:	
20			
		GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA	50
		CATTGACAAG TACAAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA	100
25		GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT	150
			. 157
		CCATGAA	15/
		(A) THEODYNATON FOR SEC ID .59.	
20		(2) INFORMATION FOR SEQ ID :59:	
30		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 252 base pairs	
	•	(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
. 35		(D) TOPOLOGY: linear	
		(xi) SEQUENCE DESCRIPTION: SEQ ID :59:	
40			
			5.0

••	CTTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT	100
	GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT	1,50
5	TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG	200
	AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA	250
•	CA	252
10	(2) INFORMATION FOR SEQ ID :60:	
-	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :60:	
	GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC	50
25	GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG	100
	AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTTCAACTT	150
	TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA	198
30	(2) INFORMATION FOR SEQ ID :61:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 229 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

	.•	GAGGTGGCAT TATGTGAGAC AGCATTTGGT TAGGGAGTGC CAAGCATTCT	50
		ACAGCATTTG ATGGTGGAAA TAGTCATGCT TTTTATTTCT GCTCTCTAGG	100
5	·	AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAAGGTC	150
		CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA	200
10		GAGTGCTTCT CATACACCTT CAGGAACCC	229
10		(2) INFORMATION FOR SEQ ID :62:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 181 base pairs	
15		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
20		(xi) SEQUENCE DESCRIPTION: SEQ ID :62:	
		CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAA GGGACTGAAG	50
25		AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA	100
		ACCECTTAAT GAATTTCATE ACCTTGAGGG CTAAAGATCG TTCTTCGGGC	150
30		AAGAGCTTTT GGACTGTTTT TAGAACAGAA T	181
		(2) INFORMATION FOR SEQ ID :63:	-
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 180 base pairs	
·35		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	

. 40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

.•	GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA	50
•	ATTTGGCAGA AACAAGAAAA GGACATGGGA TAACTTTTAG ATTTAAAGAG	100
5	GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA	150
	TAAGGCTACT CCACAAGACC ATTAGAAGTC	180
	70 TD 454	
	(2) INFORMATION FOR SEQ ID :64:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 120 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
		•
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :64:	
20	ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC	50
•	AGGGAACTGT GATTATTTAA AAATANGCNA GAACTTATTT CANCTGTGCT	100
25	TTAGAAANAA NTGTATACGG	120
	(2) INFORMATION FOR SEQ ID :65:	
	(i) SEQUENCE CHARACTERISTICS:	·
30	(A) LENGTH: 70 base pairs	
	(B) TYPE: nucleic acid	
,	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	4
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :65:	
,	CACATCGCTA TAATCCTTTC TGAGGACTTA AAACTTTATN CCACTTACCT	50
40	TTATGACTTT TAACAAGCCT	70

100

150

200

35

40

	(2) INFORMATION FOR SEQ ID :66:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 240 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :66:	
	TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT	50
15	ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG	100
-	GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC	150
	CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN	200
20	TCCACACC CACACGATTT AGGAACTTGG ACATGTTCCT	. 240
	(2) INFORMATION FOR SEQ ID :67:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 254 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :67:	

GGAAGCACTA CATTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT

TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT

TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT

AACCTATTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG

. •	AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA	250
	TAAG	254
5 .	(2) INFORMATION FOR SEQ ID :68:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :68:	
	AGGCACCAAA GAAACACCAA GCAATAAAGT GAAAGACTAA CCAAGATTTG	50
	ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG	100
20	TCAACAAATN NNNACAACTG AGAACCTGGG AATTCCCGCA CGGAAGACAA	150
•	GAGATAACCT CTCCAATTTA ACACCGCTAG GNTTCTATNN TA	192
25	(2) INFORMATION FOR SEQ ID :69:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 112 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :69:	
	AGCAGCGNNN NNNNTNNAAA CAAAAGACAG GAGCAGAGAG GCCTGAGAGC	50
	AGGAGGCGAA TTCGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC	100
40	ccccccAAG CC	112

	(2) INFORMATION FOR SEQ ID :70:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :70:	·
	AAGGGTCTCC AATTTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT	50
15	TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG	100
	ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT	150
	ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG	200
20	CAGATTTATT CCTTTAACTG ACATTTCCAT GA	232
	(2) INFORMATION FOR SEQ ID :71:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 160 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	·
30	(D) TOPOLOGY: linear	٠.
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :71:	
35	CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT	50
	TTCACTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG	100
	GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCCNGT CAGATAAGAT	150
40	TTAGGGCTGA	160

(2) INFORMATION FOR SEQ ID :72:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 182 base pairs	
· 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :72:	
	AAGGAAGACT GGTTTGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC	. 50
15	AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT	100
	CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGGAAGT TTCGATTCTT	150
	TTTTCCTCCC GTCGCAAATT CTATGTTTGG AT	182
20	(2) INFORMATION FOR SEQ ID :73:	·
	(i) SEQUENCE CHARACTERISTICS:	,
	(A) LENGTH: 168 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :73:	•
٠	CAAGAGGCAG CTGCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG	50
35	ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA	100
	CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG	150
40	ANAGGCTGCA CAATGAAA	168
***	(2) INFORMATION FOR SEQ ID :74:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 221 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :74:	
10	AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC	50
	AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCGGGGTT	100
15	GTATACCACA CCCCGGGCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA	150
	ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC	200
20	NCTNTCCCTN NAATAAATTN C	221
20	(2) INFORMATION FOR SEQ ID :75:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 127 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :75:	
	AGACTGNTTG GGTCATCCGA GATCATTAAA AATGNCTGAC CCTAACAATA	50
35	GGCACAAAAA TAAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT	100
	TAGAAAAAA CAGGGCCTTG AGTTCTG	127
40	(2) INFORMATION FOR SEQ ID :76:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 180 base pairs	

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :76:	•
	The second secon	50
	AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACA TTTCAAAACC	30
10	TOTAL	100
	CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAATGACC	
	TOTAL CACTUTTICA TTACAATATT	150
	ACAAAATTAA TACTACCAAA TCATTACTGA GACTCTTGCA TTACAATATT	
	THE TAXABLE TRANSPORTED TO THE TAXABLE TO THE TAXAB	180
15	TGGAGAGTAG GTGAAGAAAA TNTAGACCGA	
	(2) INFORMATION FOR SEQ ID :77:	
	(2) INFORMATION TON DEE 05	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 142 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
25		
	and ID +77.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :77:	
	GATTAANNNN NNNGCACCON NNATTACTGG CACAGCTGGT GAATATTTTC	50
	GATTAANNNN NNNGCACCCN NNAITACIGG CHOMOSTOS	
30	GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAAACTG	100
	GTGGACTTTT GACTAGTGGA COLOGICA	
	TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC	142
	TCACTITAGE CHOMINETED IN	
35	(2) INFORMATION FOR SEQ ID :78:	
33	(2)	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 124 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :78:	
	GGCCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC	50
5	ANGGAAANTA CACCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT	100
	CTGNCCCCC CNNNGNCCCC CCCG	124
10	(2) INFORMATION FOR SEQ ID :79:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 171 base pairs	
	(B) TYPE: nucleic acid	•
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :79:	
	AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTTCA	50
25	TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTCGTGG GTGGATGTAT	100
23	NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT	150
	TTAAGNAAAN GCCNTTTTAA G	171
30	(2) INFORMATION FOR SEQ ID :80:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 98 base pairs	
	(B) TYPE: nucleic acid	•
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :80:	

-•	CGACAGTGCC GTGNGGGCAC CATGGCACCT NGACCACGGG CNCCTAAG	90
	(2) INFORMATION FOR 2 ID :81:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 108 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
·	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :81:	
15	CCTCAACAAG TGCGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG	50
	CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT	100
	CAACATCA	108
20	**	
	(2) INFORMATION FOR SEQ ID :82:	
	The state of the s	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 180 base pairs(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) 1070b001. 12cu1	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :82:	
	ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC	50
35	CCT MAATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA	100
	GAATGTCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACAACAACA	150
	ACGCCTACGA AATTCTAAAT TCAGAAGGAA	180
40	(2) INFORMATION FOR SEO ID :83:	

(i) SEQUENCE CHARACTERISTICS:

	(-,	
	(A) LENGTH: 199 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	CDO TD .93.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :83:	
10	GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT	. 50
	GGCTTCTGAT CGCCATCCTT GAACAGGCA AAGGTGGCCT CACCAGGGCA	
	CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC	100
	CGATGCAGCT GCCATGCGCG CCAGAATTOAC CCAATGCGCT	
15 .	GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC	150
15	GIIGGACGOA IOIII	
	CTTCTTAATA AACACCTCCT CGCCAACTGC GACGACCACA ATCACCGTA	199
	(2) INFORMATION FOR SEQ ID :84:	
20		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 214 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	DECENTED PROPERTIES. SEC. ID . 94.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :84:	
30	CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA	50
	CITCOGIAGI GCCGCCGIGO ICCC	
	CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA	100
		•
35	GGGGAGAGA AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG	150
	CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATTT	200
	NACNGAATAC AACC	214
40		
	(2) INFORMATION FOR SEQ ID :85:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: base pairs	
•	(B) TYPE: r eic acid	
	(C) STRANDE. ESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :85:	
10	·	
	CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC	50
	AGTACCTGGG CATGTCCTGT GATGGCCCCT	80
15	(2) INFORMATION FOR SEQ ID :86:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :86:	
·	GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC	50
30	CCTGAAATAC GCGCTTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT	100
30	CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT	150
	GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTTA TTACTCTGTT	200
35	TCTTTTAATG	210
	(2) INFORMATION FOR SEQ ID :87:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 102 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :87:	
	CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT	50
	ATTTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA	100
10	CA	102
	(2) INFORMATION FOR SEQ ID :88:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 275 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	TOURNER PRESENTATION. SEC ID .88.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :88:	
25	GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT	50
	ACGGGCAGTG AGAACATTAT CTGTATAACA GGAACTGTGA TTATTTAAAA	100
20	ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA	150
30	TAAGTTGAAA AGAACTCAAA ATAACTAATA CAAATAAGAA CCTACGTATT	200
•	AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA	250
35	TGACACAAAT TCAAAACACG ATCAT	275
	(2) INFORMATION FOR SEQ ID :89:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 263 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :89:	
	GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA	50
	TTAATAGTAA TTATGGTTTG GNNGTAAAAT CGAGTTTCAG AATAAAATNA	100
10	AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAAGCT TTTGTTTTGT	150
•	TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTCC	200
15	TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT	250
	GCTGTGTACT CCA	263
	(2) INFORMATION FOR SEQ ID :90:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 108 base pairs(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(b) Totoboot Piness	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :90:	
30	GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC	50
	CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCCCCC CGAGGGACCC	100
35 .	CTTTGAGA	108
	(2) INFORMATION FOR SEQ ID :91:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 206 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

· 5	(xi) SEQUENCE DESCRIPTION: SEQ ID :91:	
	GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
	ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
10	TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG	150
	GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT	200
15	TAATAA	206
	(2) INFORMATION FOR SEQ ID :92:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :92:	
	CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
30	TGGCTTTGGC TGATAGATTT GAAGAGACCT CAATTACGTT TTTCAGGAAT	100
	GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG	150
35	GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
	AATAAANNNG	210
40	(2) INFORMATION FOR SEQ ID :93:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

. •	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :93:	
		50
	AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAAACT AACCTAAAAG	50
10	TO THE PARTY OF TH	100
	GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA	100
	AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT	150
	AACATGGCGA AAGGAGCTCT CTCTTTCCCC CONGIOTATIO	
1.5	GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG	189
15	GCATTICAC CACATAGATO TOCIMOTOS	
	(2) INFORMATION FOR SEQ ID :94:	
	(2) 2	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 160 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :94:	
	TO THE STATE OF TH	50
	GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG	50
30	CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC	100
	CACAATGTGG CAGGGCCTAG CIGCTACAAA GAAGACAATT TAAGAATATTA	
	TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN	150
	TORREGORIO MONIBILITO CITO CITO CITO CITO CITO CITO CITO C	
35	GTCATTTAAT	160
	(2) INFORMATION FOR SEQ ID :95:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 171 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :95:	
	TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT	. 50
	AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT	100
10	AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAA NTATAGTTTT	150
	TAAGGAAACT ACAGAAGGGA T	171
15	(2) INFORMATION FOR SEQ ID :96:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 131 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :96:	
	GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT	50
	TTCCCCAACC TTTTTATTCG CGAAGAAACT CCAGTTGTTA ACTTTTTGAG	100
30	AGTTTTTTT GGCAAAAGAA CTNCATTTAN C	131
	(2) INFORMATION FOR SEQ ID :97:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 279 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

		DESCRIPTION:	SEO	TD	:97:
(xi)	SEOUENCE	DESCRIPTION.	250	10	

	(xi) SEQUENCE DESCRIPTION: SEQ 15 1511	
	GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA	50
· 5	GTAAAGTTAA GGCACTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA	100
	CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN	150
10	TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC	200
10	ATANTGTATT GATGATCTGC TGTAACTTTG AGAAGCTTCC TGAAGCTCNT	250
	TTTGAATAAA TTTATNGAAC TTATGAAGA	279
15	(2) INFORMATION FOR SEQ ID :98:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :98:	
	GTGAGTCTTT CTTCAACTAG GGGAATGTTT CCAGGGCACG CCAGGCCTCA	50
30	CTCACGCAGG CCTCCGCGAC AACTGTTCAG CACTGACTGA GGATGAAGTG	100
30	AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA	150
	CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT	200
35	GACGAGACCA GGACCCTTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA	250
	AACTCCAGGG CCTCCA	266
,	(2) INFORMATION FOR SEQ ID :99:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	() CROUDING DESCRIPTION, SEO ID .99.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :99:	
	GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA	50
10		
	ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA	100
		15/
	TATGTATATA TAGAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA	150
15	GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTTAC TCTTTGGGTA	200
13	GIGGIIACCC CIGGIMACCC COMMINGUM CITAMIC COMMINGUM	. —
	CGTATT	206
	(2) INFORMATION FOR SEQ ID :100:	
20	· · · · · · · · · · · · · · · · · · ·	•
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
		•
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :100:	
30	CGCAACTNTC NCTAAACATC CAGTTTTCTA ATNTAATAAA AAATGGCAGT	5
	AATTATCCTC ACCTCTCAGG GAA	7.
		•
35	(2) INFORMATION FOR SEQ ID :101:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs	
•	(A) LENGIN: 100 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	:101:
------	----------	--------------	-----	----	-------

	(xi) SEQUENCE DESCRIPTION: SEQ 15 .101.	
	GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC	50
· 5	ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT	100
	ACTGCCCC	108
10	(2) INFORMATION FOR SEQ ID :102:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :102:	
	GAATTATCAA ACCATCNTTG CTGACATTAA TTTTCCAGCT TTGATCTTAN	50
	NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTTCTCA LACGATNTAT	100
25	CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT	150
	TCAATATAAC ANAAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN	200
30	CTGTTAACTG	210
	(2) INFORMATION FOR SEQ ID :103:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 76 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

	CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT	50
	GTCACCAAAA TTTCTTTCCA AAAAAA	76
5	(2) INFORMATION FOR SEQ ID :104:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 167 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :104:	
	CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA	50
	AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA	100
20	CCGATTGAAT GGTTTTTTAA GAATAAAAA GAAGTCTGAT ACTGAACTAC	150
	AAGTCGCAAG GAACATC	167
25	(2) INFORMATION FOR SEQ ID :105:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 122 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :105:	
	TATCTGCATA TCTAAACATA GAAAAGCACA ATAAAAAACAC ATATCATAAC	50
	CTCACGGGAC CACCATCATA CAGCAATTTG TCATGATCAA AAGAAACATC	100
40	ATTACTCCTC CCATAACTCT AT	. 120

(2)	INFORMATION	FOR	SEQ	ID	:106:
-----	-------------	-----	-----	----	-------

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 255 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :106:	
	GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT	50
15	GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCAACCC TCACAGACTC	100
	THE PARTY OF THE P	15/
	ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA	150
	GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG	200
20	GAIGAIGIIA IIIACAAGIG IIIAIGGAIC ACIIGAAGAA ACIIGCIGIG	200
	TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA	250
	AATAA	25
25 .	(2) INFORMATION FOR SEQ ID :107:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 227 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
3.5	(xi) SEQUENCE DESCRIPTION: SEQ ID :107:	
35	(X1) SEQUENCE DESCRIPTION: SEQ ID :107:	
	GGACGTGAAT TGGTGGAATA TTTACAAAGA AAACTGTTTT CTCAAAACAC	5
	CONCOLUMN TOURS OF THE COMMISSION OF THE COMMISS	•
•	TGTTCATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA	10
40		

AGAACTTGCA TTTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT

. •	AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT	200
	ATACCAAGAN ACANTTATGT GGTAAAT	227
5	(2) INFORMATION FOR SEQ ID :108:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 162 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :108:	
	GAAAAATNGC ATGAAAGAAG ACTCTTNNNN NGCCATACCA TGGTACAATA	50
	ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA	100
20	Aloninani momento indicator con la companya de la c	
20	CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAA ATAGNAAAAA	150
	AAAAAAATAA CA	162
25	(2) INFORMATION FOR SEQ ID :109:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 154 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :109:	. -
33	(NI) Caronica carried and the same of the	
	AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA	50
	AAATAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC	100
40	A MARCA MOCANO, COCA CA AMBIC. CACCOCTACO, COCCATACTO, ATCATTOATT	150

		GTTT	154
		(2) INFORMATION FOR SEQ ID :110:	•
5		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 182 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
•		(D) TOPOLOGY: linear	
10			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :110:	•
15		ATGTGCCAAG TAAAAAATCA ATTNGTNGCC TTTTTCCATT NCGCGGACAC	50
		CCATAGGCAC CAAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG	100
20		AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT	150
20		GCACTCCTTG TTAATAACAA TACACTATAT CA	182
		(2) INFORMATION FOR SEQ ID :111:	
25		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 94 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
30		(D) TOPOLOGY: linear	
		(xi) SEQUENCE DESCRIPTION: SEQ ID :111:	·
35	,	GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA	50
		CNTCAAAACC AATGGTAGAA CATCACATTT CAAACTGCAA ACCA	94
		(2) INFORMATION FOR SEQ ID :112:	
40			
•		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 92 base pairs	

• •	(B) TIPE: Nucleic actu	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
·5	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :112:	
		•
	TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT	50
10		
	GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT	92
	(2) INFORMATION FOR SEQ ID :113:	
	(2) Internation for SER ID 12201	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 152 base pairs	-
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
٠		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :113:	
·25	GATTGTTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG	50
-23	GATIGITIT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG	50
	TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG	100
	Transcriber Charles and Charle	100
	ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG	150
30		
	GG	152
	(2) INFORMATION FOR SEQ ID :114:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 182 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

••	(xi) SEQUENCE DESCRIPTION: SEQ ID :114:	
	TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTTCAGTG	50
5	TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG	100
	GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA	150
10	TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA	182
10	(2) INFORMATION FOR SEQ ID :115:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 182 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :115:	
	GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC	50
25	TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC	100
	AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC	150
30	TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT	182
	(2) INFORMATION FOR SEQ ID :116:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 227 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TODOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

. •	GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTC ATAAANTAAC	50
	ATACAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA	100
5	TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT	150
	ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA	200
10	TGGAAATAAG CTAGCTACGC TCAATGC	227
	(2) INFORMATION FOR SEQ ID :117:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :117:	
	CGAGAGATTG GTAATGAGGA AGCAATTTGG AGGGGNGGAA GCTACAANGA	50
25	NNNNGGGAAT TACAACAATC AGTCTTCAAA TTTTGGACCC ATGAAGGGAG	100
	GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC	150
30	TTGCAAAACC ACGAAACCAG GT	172
	(2) INFORMATION FOR SEQ ID :118:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	•
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

PCT/GB93/01467

	AATGATGGAA GCAATTTTGG AGGTGGTGGA AGCTACAATG ATTTTGGAAT	50
	TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG	100
5	GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG	150
	AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG	200
	GCAGAAGATT	210
10	(2) INFORMATION FOR SEQ ID :119:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 95 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		•
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :119:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID :119:	
	GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT	50
25	TTGGTGAGGA ATTAGCAATI TCTTGCCAAA GAAAATTGAT TCTGC	95
	(2) INFORMATION FOR SEQ ID :120:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :120:	
	GGAGTATTTN AANNTTTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA	50
40		
	ጥኔሮጥሮሮምምርሮ አልጥልጥልሮሞም አልጥሮሮምምጥም ምጥሮምሮዊምንል አጥጥጥምምምር	100

•	TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTT ATTAACTGCT	150
	TCCAGAAACC GTAACAGG	168
5	(2) INFORMATION FOR SEQ ID :121:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 231 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :121:	
	GGAGTATTTA TCTTTCAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA	50
	CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTTCN NCTGTTTTTC	. 100
20	AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA	150
	ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA	200
25	ATACATACTT CGGTGACNTT ATGCATCATG A	231
	(2) INFORMATION FOR SEQ ID :122:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 174 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :122:	
	TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT	50
40		100
	SAMOMOMOSO DUNCTUNITATUS (2012ALIMATI) (C. OXATALIXI LAKITIALIALIXI LAKITALI	ושוג

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :127: TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG 50 10 AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTCAG CAACTTGACA 100 TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT 150 160 15 **AGGAAAACCA** (2) INFORMATION FOR SEQ ID :128: (i) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :128: GCCCACAACT TACATCCTCA TTATTGGCGC CTACAAACTC AACTACGAAC 50 30 ACACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTACTCGGCT 100 ACCCCTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC 150 35 (2) INFORMATION FOR SEO ID :129: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs (B) TYPE: nucleic acid 40 (C) STRANDEDNESS: double (D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID :129:	
	AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTTCCGAAG	50
5	CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA	100
	GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA	150
10	TGAAAAACCC AAAACAGTTA CGANGCTAAT CC	182
	(2) INFORMATION FOR SEQ ID :130:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 219 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :130:	
	GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT	50
25	TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC	100
	TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT	150
30	TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA	200
	TGCTTACTTC AAGAAGAAG	219
35	(2) INFORMATION FOR SEQ ID :131:	·
J 5	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 181 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
	· · · · · · · · · · · · · · · · · · ·	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :131:	
	AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA	50
5	GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT.	100
	CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT	150
	AGAACATCGT TAACGGAATC ACAGATATAT C	181
10	(2) INFORMATION FOR SEQ ID :132:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 188 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :132:	
	GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT	50
25	GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG	100
	TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG	150
20	CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC	188
30	(2) INFORMATION FOR SEQ ID :133:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 190 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

	 GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC	50
	TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT	100
5	CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTCAC AGAAGCTCTG	150
	TGACTTGGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC	190
10	(2) INFORMATION FOR SEQ ID :134:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :134:	
20	ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC	50
	AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC	100
25	CAGGGTCCAT TTAACTAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT	150
	GTCCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA	200
30	TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG	235
	(2) INFORMATION FOR SEQ ID :135:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 147 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

PCT/GB93/01467

. •	GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT	50
	ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC	100
· ₅	AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG	147
	(2) INFORMATION FOR SEQ ID :136:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 171 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :136:	
	GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA	50
20	CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG	100
	NTCCCANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA	150
25	CTNAGAATGC GGAGGAGATC T	173
	(2) INFORMATION FOR SEQ ID :137:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 159 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	-
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :137:	
	ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT	5
40		
	TTCTCCTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG	10

	.•	TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTTGAGTCT	150
		GTAAGTAGG	159
5		(2) INFORMATION FOR SEQ ID :138:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 179 base pairs	
		(B) TYPE: nucleic acid	
10		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
15		(xi) SEQUENCE DESCRIPTION: SEQ ID :138:	
		CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAACTA AAACTACGAC	50
		NCACTCACAA TCGCTCATAA TCTCTTNAGG ACTTCAAACT NTCTCTNTGA	100
20		NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCCNTGTNC	150
		TNCGGGAGAA CTCTCTGTGC TGTACCAGT	179
25		(2) INFORMATION FOR SEQ ID :139:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 177 base pairs	
		(B) TYPE: nucleic acid	
30		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
35		(xi) SEQUENCE DESCRIPTION: SEQ ID :139:	
		GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC	50
40		TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG	100
70		ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA	150

٠ .	AAGGCGATGA CCAGAGCCGC AAGGCNG	177
	(2) INFORMATION FOR SEQ ID :140:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :140:	
15	GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTTGTGA	50
	CTTATACTGT CTNTGTCAGT TA	72
20	(2) INFORMATION FOR SEQ ID :141:	
20	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 62 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(with groupings programments, ero in (14).	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :141:	
	GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTTA AGTATTNGTT	50
	TTAGTACGNA AA	62
35	(2) INFORMATION FOR SEQ ID :142:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 127 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

•	(xi) SEQUENCE DESCRIPTION: SEQ ID :142:	
	ACCAGINNNI GATIGGIAAA IGGGAAATAI AATIGATICI GATCACICII	50
5	GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTTA AGAAAACGAG	100
	TTAAGTTTAA CAGTTTTGCA TTACAGG	. 127
10	(2) INFORMATION FOR SEQ ID :143:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :143:	·
	AATATAAAAG ACAGCAGTTT CACATTTCAC ATATTTGAAA AACATTTCAA	50
25	AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT	100
23	GACCACAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA	150
	ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT	198
30	(2) INFORMATION FOR SEQ ID :144:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 174 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :144:	

	AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG	100
	TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG	150
5	AAACTGCTTT GTATCTGCTT TGNA	174
	(2) INFORMATION FOR SEQ ID :145:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 156 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		:
	(xi) SEQUENCE DESCRIPTION: SEQ ID :145:	
20	GAGAAATAGT ACTTTAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT	50
	AAGATTCATA AAATGTACCT TTTTTGATTG TTTTGTTCTN GAGTTTTCGA	100
	TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA	150
25	TTTTGG	156
	(2) INFORMATION FOR SEQ ID :146:	
	(i) SEQUENCE CHARACTERISTICS:	
. 30	(A) LENGTH: 151 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :146:	
•	AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG	50
40		100

	 TAGATAGTAT ACTITACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT	150
	T	151
. 2	(2) INFORMATION FOR SEQ ID :147:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :147:	
	CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAACTC	50
20	CAGGTAANNT GGTTTGATCT GATCGATTTG GCTGCATACT TTCGGTACGT	100
20	ATAACATTCT AAACTTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG	150
	TAAAATTTTA AAAGTTAAAG TACTAGC	177
25	(2) INFORMATION FOR SEQ ID :148:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 148 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :148:	•
	GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT	50
40	TGGAAATTGG CTGTTTTGTT AAAATATATC TTTTAGTGTG CTTTAAAGTA	. 100
	GATAGTATAC TTTACATTTA TAAAAAAAAT CAAATTTTGT TCTTTAAT	148

	(2) INFORMATION FOR SEQ ID :149:	
5	(i) SEQUENCE CH; ACTERISTICS:(A) LENGTH: 204 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :149:	
	AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG	50
15	GTTGGAAATT GGCTGTTTTG TTAAAATATA TCTTTTAGTG TGCTTTAAAG	100
	TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTATT	150
20	TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA	200
20	ATCC	204
	(2) INFORMATION FOR SEQ ID :150:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(b) TOPOLOGI. Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :150:	
35	AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA	50
	TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT	93
40	(2) INFORMATION FOR SEQ ID :151:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 151 base pairs	

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
5	·	
	· and the state of	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :151:	
	AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT	50
10	ANICOMON ANAMIONIO NOMOZOZNOG IZIZIZIO ZA	
•	ACTITGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC	100
	CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAAC CAGGAAGGTG	150
15	T	151
	70 TO THE STATE OF	
	(2) INFORMATION FOR SEQ ID :152:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 109 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :152:	
	(XI) SEQUENCE DESCRIPTION. SEQ ID .132.	
	TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT	50
30 -		
	CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA	100
	TGTAGCCTC	109
35	(2) INFORMATION FOR SEQ ID :153:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 136 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :153: AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50 5 TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100 136 AGGAAAAGGG GAAAAAAACC CATAATGGGC CTAAAA (2) INFORMATION FOR SEQ ID :154: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double. 15 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID :154: 20 CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50 CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100 25 150 TCAAGATGAG TATACGCATC TATCATTCGA ATTGTGTCAT TAATTTGTAG 160 GGCCTCATTG (2) INFORMATION FOR SEQ ID :155: 30 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double 35 (D) TOPOLOGY: linear

	ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT	100
	TTTTAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT	150
5	GACTTCATGC TTACTGTAAA GTGGAAGTTG AGATATTTTA A	191
	(2) INFORMATION FOR SEQ ID :156:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :156:	
	CAACTGAACG CTTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN	50
20	TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT	100
	GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCAGTG	139
25	(2) INFORMATION FOR SEQ ID :157:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :157:	
	GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA	50
	CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT	100
40	TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA	150

	AGCACCCGCA AATTTACCTT TG	172
	(2) INFORMATION FOR SEQ ID :158:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 93 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		٠
	(xi) SEQUENCE DESCRIPTION: SEQ ID :158:	
15	GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT	50
	CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG	93
	(2) INFORMATION FOR SEQ ID :159:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 102 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :159:	
	GNATTTTTT ATTGATATAT CATAGTTGTA CAAACATTTG GGAGTNCANG	50
	TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC	. 100
35	CA	102
	(2) INFORMATION FOR SEQ ID :160:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 205 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :160:	
	GCTTTTNNNN NNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA	50
	TAGAAGCAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT	100
10	ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT	150
	ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA	200
15	GCGGA	205
	(2) INFORMATION FOR SEQ ID :161:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 150 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	· · · · · · · · · · · · · · · · · · ·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :161:	
30	AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA	50
30	AGTTGTTTTC CATATAAAA ANNNNNNTGA TTTTTAAAAA ACTAANNAAC	100
	TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA	150
35	(2) INFORMATION FOR SEQ ID :162:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 77 base pairs(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(D) IOLODOGI, ITHERT	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :162:	
	TATTCAAAAG AAAAACATGG GTAAAAATGA TAGTGTTAAA TCTTGGCTCT	50
· 5	GTGTACATAG ATAGATACCT GTTACAG	77
	(2) INFORMATION FOR SEQ ID :163:	·
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 182 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :163:	
20	GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT	50
	TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT	100
25	AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT	150
25	CAAACTGACA TGCTACAGAA ATGTCTTCCA AA	182
	(2) INFORMATION FOR SEQ ID :164:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 182 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
35		·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :164:	
40	GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA	50
	TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC	100 .

	AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT	150
	CAGATTCACA GACATTTGCA AAACAGAAGA TG	182
5	(2) INFORMATION FOR SEQ ID :165:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 119 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :165:	
	GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT	50
	GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG	100
20	TGTATATAAA AAGAAATAA	119
	(2) INFORMATION FOR SEQ ID :166:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 193 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :166:	
35	GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTCC AAACACATAG	50
	GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG	100
	GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA	150
40	AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG	193

.. (2) INFORMATION FOR SEQ ID :167:

5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 185 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :167:	
	GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG	50
15	GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT	100
	GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT	150
20	TAAATGGACA GTTTATAAAG TGTTCTGGA GCCGA (2) INFORMATION FOR SEQ ID :168:	185
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :168:	
	GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG	50
35	TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG	100
	ATTTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA	150
	ATTTTTAAAA ATA	163
40	(2) INFORMATION FOR SEQ ID :169:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs(B) TYPE: nucleic acid

_	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :169:	
10	AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTTCAGATG CCACCGTATA	50
	GCAAAGGGTG AACATGTTTT CAACCCTTTA ACTTTTTACG GTGTTTGAAG	100
15	ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG	150
	CAGATTTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC	200
20	CT	202
20	(2) INFORMATION FOR SEQ ID :170:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
25	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) Totoboot. Tricur	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :170:	
	TCAGGGAACC AAAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT	50
35	TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC	100
	ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT	150
40	GGTGCCCAGG GCTGTAAA	168
40	(2) INFORMATION FOR SEQ ID :171:	

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 144 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :171:	
10		•
	AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA	50
	GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC	100
	COMMITTATO ACACTIACAT TIMONOTOGA COTTIACIAA CONGGONAMO	100
15	TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT	144
	(0) TNDODWATON DOD OD TO 100	
	(2) INFORMATION FOR SEQ ID :172:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 91 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :172:	
30	ACCCACAGNN NNNACCTAGA GGCCCAGCGC CCAGAGAGGC ACGTAGAAAT	50
30	GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A	91
	Total Control	31
	(2) INFORMATION FOR SEQ ID :173:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 204 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
40		

••	(xi) SEQUENCE DESCRIPTION: SEQ ID :173:	
	GATTTTTAA TGGGTNGCCT CTTTTAGCTT GGAATATTAC GTTTACTTTA	50
. 5	ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT	100
	GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTTT GGTGTGATTA	150
	CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA	200
10	TGGA	204
	(2) INFORMATION FOR SEQ ID :174:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 241 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :174:	
25	GTAAATTTCA CTACATCTTT TNNTNTGACT TTCATGCATT TCTCATACAT	50
	TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA	100
30	ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTTNAGG	150
30 .	ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT	200
	TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G	241
35	(2) INFORMATION FOR SEQ ID :175:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

•••	(xi) SEQUENCE DESCRIPTION: SEQ ID :175:	
_	GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT	50
.5	TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT	100
	AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC	150
10	TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT	200
	TTGGCCCTTT T	211
15	(2) INFORMATION FOR SEQ ID :176:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 252 base pairs (B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :176:	
25	AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG	50
	NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN	100
30	TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA	150
	AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTTCT GACCTATGAT	200
	AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA	250
35	AT	252
	(2) INFORMATION FOR SEQ ID :177:	
40	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 279 base pairs(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
· 5	(xi) SEQUENCE DESCRIPTION: SEQ ID :177:	
	GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA	50
10	GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG	100
	TTGCAGCCAA TCTTCTCAAA GCAAACCGAC TTCCTAACAA CTNTCTACAT	150
15	CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA	200
	TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC	250
	ATCTGAAGAT ACCAGCTTCA AATACTAAT	279
20	(2) INFORMATION FOR SEQ ID :178:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 157 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :178:	
	TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC ACAAAAACAG	50
35	ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTTG GTGGGTGGTC	100
	GTTCTCAATT TATAAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT	150
	GTCAGGA	157

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID :179:

WO 94/01548

106

_	(A) LENGIN: 39 Dase pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
_. 5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :179:	٠
	(XI) SEQUENCE DESCRIPTION: SEQ ID :1/9:	
10	GATAATGCAA CTTTTGACAG GAAAGCGCGA TTTTACTAT	39
	(2) INFORMATION FOR SEQ ID :180:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 157 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(with Grouping Programmes and an area	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :180:	
	GCAAACTCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG	50
25		
	GACTTAAACT CTACTACACT AATACTTTTT GATGACTTCT AACAAGCCTC	100
	GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG	150
30	TACCACA	157
		157
	(2) INFORMATION FOR SEQ ID :181:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 195 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		
		•

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

PCT/GB93/01467

••	CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA	50
	CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC	100
, 5	ATTCTGGTAA AAACTGGAAG ATGACCCTAA ATTTTGAAGT TGATGATGTG	150
	CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT	195
	(2) INFORMATION FOR SEQ ID :182:	
10		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 146 base pairs	
	(B) TYPE: nucleic acid	
•-	(C) STRANDEDNESS: double	-
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :182:	
20		
	CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT	50
	GTTTGTCCTT CAAATGGGAC AATTTGAGGA ATGCTTTAGG CAGAGGACTC	100
25	AGATGACAGA GCGCCAACCA CCCACAATAG AAACCTGCTC ATCACA	146
	(2) INFORMATION FOR SEQ ID :183:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 50 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) TOPOLOGI: Timear	
35		
55		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :183:	
	TAGAGGAATA GGGNNNGNGA CGCCCCNAGT TGTAGGGACG GACGGAGGAC	. 50
40		
	(2) INFORMATION FOR SEQ ID :184:	

(i) SEQUENCE CHARACTERISTICS:

·	(A) LENGTH: 248 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
		•
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :184:	
10	(12) 52202102 5200101 510011 502 50 50011	
	ACGNITACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC	50
	AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG	100
15	CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT	150
15	CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT	150
	GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA	200
	·	
	TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT	248
20		
	(2) INFORMATION FOR SEQ ID :185:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 113 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		
30		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :185:	
	AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT	50
35	ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG	100
	AACGTGGCTT TCT	113
•	AACGIGGCII ICI	113
	(2) INFORMATION FOR SEQ ID :186:	
40		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 148 base pairs	

	(b) IIIb. naciele acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
,		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :186:	
	GGGCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCG	50
10		
	ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC	100
	ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC	148
15	(2) INFORMATION FOR SEQ ID :187:	
	(2) INTOIGHTION TON SEQ ID .10/.	
	(i) CROUPLOR OUT DE COMPETANTE	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 248 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :187:	
	•	
	TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG	50
	TOTAL MONOCONTI IMMOGNITA MANICOCACI NGCCATACLG	. 50
	TARCATCATA CCACCARCCA TACCOTACCA TCARRATTE ATORES	
20	TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA	100
30		
	GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT	150
	\cdot \cdot	
	AATTAAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC	200
35	TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC	248
	(2) INFORMATION FOR SEQ ID :188:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 146 base pairs	
- -	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :188:	
	TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTCA	. 50
	GTTTAATACA TAAGTGTCCA ATAATAATGT CAACCCTCCC TCGCCACAGC	100
10	CAATAATTTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT	146
	(2) INFORMATION FOR SEQ ID :189:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 81 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :189:	
25	ATTTACCACA AGGGACGATT TCCACACCAA CCCCAAAAAT GTCCCCTATG	50
	ACGACGAAAT GTGTATTTGA AACAGCTCTG A	81
	(2) INFORMATION FOR SEQ ID :190:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 136 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :190:	
70	ARCTACAGO TOOTGOTGOA AAAATGATTG TAATGNOTTO TOATATGOAA	50

. •	GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTTG TGAGCTTCCT	100
	GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA	136
5	(2) INFORMATION FOR SEQ ID :191:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 152 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :191:	
13	(112)	
	AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA	50
20	ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA	100
20	AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA	. 150
	CA	152
25	(2) INFORMATION FOR SEQ ID :192:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 65 base pairs	
	(B) TYPE: nucleic acid	•
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
,		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :192:	
	TAAGCGAGGN NGTCTTTGAT TGCGTAGTAA GGTAAAGACG ATTTTATAGA	50
	ATNAAGGTGA TTCCT	6
40	(2) INFORMATION FOR SEQ ID :193:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 9 base pairs(B) TYPE: nucleic acid

	(C) STRANDEDNESS: GOUDTE	
5	(D) TOPOLOGY: linear	
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :193:	
10	AGGACCCAAA CTACCTTATT GCATTTGAAG TTTTACTTAT NCTATTATAA	50
	TCTAAGAGCC CACCCAACAA GGCACTACAC ATAGATGCTC ACACTCTATA	100
15	GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG	150
	CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC	200
20	TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA	249
20	(2) INFORMATION FOR SEQ ID :194:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 194 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :194:	
	GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG	50
	GGAAAGGGTG CCTCATCCCA GCAACCTATO CTTCTCCATC	
35	TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC	100
	GCTGCATATG TGACTGTCAT GAGATCCTAC TAGATGATCC TGACTAGAAT	150
4.5	GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT	194
40	(2) INFORMATION FOR SEQ ID :195:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 121 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :195:	
10	GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA	50
	TTTAAGTCAC ACACATAGTT AACAACNCNC GTNGCGTGCA ATAAATACCA	100
15	CATCCTTINA TATGNNCNGN A	121
,	(2) INFORMATION FOR SEQ ID :196:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 175 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :196:	
30	GGGCTTCNNN NNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC	50
	CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT	100
	AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA	. 150
35	TTGTGACCAC AAGTCTTGTT TCTTG	175
	(2) INFORMATION FOR SEQ ID :197:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 273 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

· 5	(xi) SEQUENCE DESCRIPTION: SEQ ID :197:	
	ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG	50
	AATCAGAGGT ATCAATGAAA TGAGCCCAAA GGTTCGAAAG CTCGCAACTT	100
10	CTTCACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT	150
	ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA	200
15	ARTGACTART CTACARGENT GTTATGCARA ATARATARGA ARCGACTTGC	250
	TTACAGATGC NTTTTAATTG TGG	273
20	(2) INFORMATION FOR SEQ ID :198:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	,
	(xi) SEQUENCE DESCRIPTION: SEQ ID :198:	
30	GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT	50
	GNTATA	56
35	(2) INFORMATION FOR SEQ ID :199:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 132 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :199:	
	GGACGCTGNN NNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG	50
5	GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC	100
	CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA	132
10	(2) INFORMATION FOR SEQ ID :200:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 284 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :200:	
	AAACTTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC	50
	GACATTTCAA TCGNACACAA ANTTAAAAAA TAAAACAAAT TTTAAAAAAAC	100
25	CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAAATTCA	150
	GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG	200
30	CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN	250
	TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT	284
35	(2) INFORMATION FOR SEQ ID :201:	
ŞO	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 106 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	••	(xi) SEQUENCE DESCRIPTION: SEQ ID :201:	•
		CCTGACACCA ATTTCGCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA	50
5		AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTTNT	100
		CTTGNT	106
		(2) INFORMATION FOR SEQ ID :202:	
10		(i) SEQUENCE CHARACTERISTICS:	٠
		(A) LENGTH: 270 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
15		(D) TOPOLOGY: linear	
		(xi) SEQUENCE DESCRIPTION: SEQ ID :202:	
20		CTTTGGAAAA CAAACATTTN TTATTACTGA AATAGCAAAA ATCATTCTAC	50
	. '	ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA	100
25		AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCCTAAGT GTTTGCTAAT	150
•		TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA	200
		CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT	250
30		CATTACTCTA ACTGTTAATC	270
		(2) INFORMATION FOR SEQ ID :203:	
35		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 173 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	,
		(D) TOPOLOGY: linear	
40			

••	(xi) SEQUENCE DESCRIPTION: SEQ ID :203:	
	AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA	50
5	AGCTTATTGA TTAGGTGATA TTTTTATAAC AATTGAAAGG GCAATATCAA	100
	ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAAACTG ATTTTTACTT	. 150
	TACAAAANNG NAATTTGCAA TTA	173
10	(2) INFORMATION FOR SEQ ID :204:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 164 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		
20		•
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :204:	
	CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN	. 50
	·	
25	ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT	100
	CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT	150
•	CCGCNCAAGA AGAAGAACCI GCIGCIICAI ACAACACGGG GAGGCCCIGI	150
	CATTAACATT ANTT	164
30		
	(2) INFORMATION FOR SEQ ID :205:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 99 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

	GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG	50
	AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT	99
5	(2) INFORMATION FOR SEQ ID :206:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 118 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :206:	
	GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC	50
•	ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT	100
20	TGGGGTTAGN TGTTCNAA	118
	(2) INFORMATION FOR SEQ ID :207:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 170 base pairs	
-	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :207:	
35	CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTTAA	50
	TAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCG	100
40	AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC	150
40	GCTATGCATA ATACCCTCAC	170

•	(2) INFORMATION FOR SEQ ID :208:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 129 base pairs	
· 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :208:	
	TTCAATGAAA TGCTTGTATA CAATGATATA ACAAAGAAAC CCTAAGACAA	50
15	CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT	100
	TTTCTCGGGG AAGTAACCCT GCCTTTGAA	129
20	(2) INFORMATION FOR SEQ ID :209:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 190 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :209:	
	CTTGGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG	50
	GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT	100
35	CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN	150
	AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT	190
40	(2) INFORMATION FOR SEQ ID :210:	
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 129 base pairs

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	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :210:	
	TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG	50
10	TCATTGAGTC ATCCTITTE CCTGCTGCTG TAAGGTTTT TTTCTTCTAG	50
	TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT	100
	GATGCAGAAC TGTTTCATAT CTAGAAATG	129
	••	
15	(2) INFORMATION FOR SEQ ID :211:	
		•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 152 base pairs (B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		•
•		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :211:	
		,
	CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG	50
	CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG	100
30		
	AAATGGAANC NNNGNGTTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT	150
		•
	GG	152
35	(2) INFORMATION FOR SEQ ID :212:	
	(i) CROUDING CUIDICEDICE	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :212:	
	CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG	50
5	TCGAAAGATG AAAACAACTA AGTTCATAAC CCCCTGCCCG CCATTGACCT	100
	CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTTACATC	150
10	NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT	186
	(2) INFORMATION FOR SEQ ID :213:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 152 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		,
	(xi) SEQUENCE DESCRIPTION: SEQ ID :213:	
25	CTTAAATGCC TGTTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA	50
	CCTTTCTCTA AAATTCCTTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT	100
	TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACTCTA	150
30	TT	152
	(2) INFORMATION FOR SEQ ID :214:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 290 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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	TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG	50
	ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACTC CCACCGTATG	100
5	TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC	150
	ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT	200
	GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT	250
10	ATTATTCAAT AGTGGAAATG ATGACTACAG CTATACCTCA	290
	(2) INFORMATION FOR SEQ ID :215:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :215:	
25	GTTTCTTCCA GTACATCCAA GTTTAAAATT ATTAGCGAAA TGGTCCATGT	50
	TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGGAAGATCT	100
30	GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC	150
	TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC	200
	TTACCTACCT CAGAGGGATT TGCGAAGCAA ACTGTTAATC TTCGAAAACG	250
35	ACCATTTACT TTTAGGATAT CAA	273
	(2) INFORMATION FOR SEQ ID :216:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 118 base pairs(B) TYPE: nucleic acid	·

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :216:	
	ATCTACGGCT AGGGAGAAC AATGTTCCTA CATATTATGG GTAGTGAGAA	50
10	CATTATCTGT ATAACAGGGA ACTGTGATTA TTTAAAATTA TGCAGAACTT	100
10	ATTTCATCTG TGCTTTAG	118
	(2) INFORMATION FOR SEQ ID :217:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 197 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	÷
20	(a) rotoboot. Tricar	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :217:	
25	GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAAGAAGA AAACAAGTCT	50
	ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA	100
30	TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAACTAAA NGNNNTGATT	150
	TACCACCAAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA	197
	(2) INFORMATION FOR SEQ ID :218:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 177 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	

. •	(xi) SEQUENCE DESCRIPTION: SEQ ID :218:	
	CTCGCGAGCA CTCGTCCGAG AGGTCCCATA CNNNNNNCC CAAGCCCCTC	50
· 5	AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAAACGCAC	100
	TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC	. 150
	TATTTTAGGC TNCNAGGTCA AAATAAA	177
10	(2) INFORMATION FOR SEQ ID :219:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 118 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :219:	
	GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA	50
25	GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG	100
	TNGGTNTCAG GGCTGGAC	118
	(2) INFORMATION FOR SEQ ID :220:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 233 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :220:	
40	GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT	50

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٠.٠	ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAACTGTA	100
	CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT	150
5	TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN	200
	NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA	233
10	(2) INFORMATION FOR SEQ ID :221:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 235 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	•	
·		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :221:	
	GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA	50
	ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA	100
25	GGCAGACTTA CCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA	150
	CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG	200
30	TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT	235
	(2) INFORMATION FOR SEQ ID :222:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 101 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :222:

	 GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG	50
	CCTTAGGAAT TGANTGAGGA CTTAAATTTC CCCNGAGGGA GAGNAGTGGA	100
5	G	101
	(2) INFORMATION FOR SEQ ID :223:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 271 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :223:	
20	ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC	50
	ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT	100
	TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT	150
25	TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA	200
	ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC	250
30	CATTCTTGAG ATACCAGCTT C	271
	(2) INFORMATION FOR SEQ ID :224:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 101 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

••	AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA	50
	ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA	100
5	T	101
	(2) INFORMATION FOR SEQ ID :225:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 141 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
٠.	(xi) SEQUENCE DESCRIPTION: SEQ ID :225:	
20	TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT	50
20	AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA	100
	GACCCTGTTA ANTITGGTGA AAATAACTTT CCANATTTCA A	141
25	(2) INFORMATION FOR SEQ ID :226:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :226:	
	ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG	50
	TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG	100
40	TTCTGTTATG TGCAAAGTAG ATTATTTCAT ATTTACTTGG TATGGAAAGC	150

	AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAA	G 200
	AAAANGCTGT TNNAAAAA	218
5	(2) INFORMATION FOR SEQ ID :227:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 209 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :227:	
	GAAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTG	G 50
	TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAG	G 100
20	CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATC	T 150
	TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNC	CG 200
25	GGGTTGGGC	209
	(2) INFORMATION FOR SEQ ID :228:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 179 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :228:	
	TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGC	CT 50
40	ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTT	AC 100

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	AGATGTAAAC AATGACACAG TTACATTTTT TTTTTAAATG GTAAAACCCC	150
	TTTTTACTGG NCNTTCCAGA ANCTTACAG	179
5	(2) INFORMATION FOR SEQ ID :229:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 184 base pairs	
	(B) TYPE: nucleic acid	•
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :229:	
	AGTTTAATCT CANNNNNNA TGTCACAAGT TATTGTAGCA GTGAAACAAT	50
20	GAGGGCATAC ACTATATNGA AAAAAAAACC TCCTCCCTNA TTCTCACGCC	100
20	AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA	150
	TACACCATCA TAAAGGNTCC TAAATTCATC TCTA	184
25	(2) INFORMATION FOR SEQ ID :230:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 140 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :230:	
	(ma) = = = = = = = = = = = = = = = = = = =	
	GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTC	50
40	TTTTTAGGTT TAGAATTTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA	100
40	GTGCAAACAT TGTTGAGTAT GTTGTCAAAC GTCTAAAAAA	140

210

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GCAACCANGG

	(2) INFORMATION FOR SEQ ID :231:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :231:	·
	CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT	50
15	CCTAAGGCAG GAAGATGGTG GCNNNTNNNG ACGAAAAAGT CGCTGGNGNN	. 100
	NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG	150
••	GGGGTAAAAG NAANATNNGA ANATGGAT	178
20	(2) INFORMATION FOR SEQ ID :232:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		٠
	(xi) SEQUENCE DESCRIPTION: SEQ ID :232:	
	GAGCCAACGC CACNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC	50
35	CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT	100
	THE SECOND THE SECOND ASSESSMENT TO THE TATAL NOTICE OF THE SECOND THE SECON	150

NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG

	(2) INFORMATION FOR SEQ ID :233:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 247 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :233:	
	ACTGTGCGAG TAGCTTNAAA ANNNNNNNN NNACTCAGTT TNATTTATAC	50
15	AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC	100
	CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG	150
	ACTITCTINAC INTICARACINA INTATTICACG TARARARCAT CACAGTGCGA	200
20	AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG	247
	(2) INFORMATION FOR SEQ ID :234:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 169 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :234:	
35	AAACACCAAA NAAANNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT	50
	GTGGACATTG GAATGTTTAC TGTTATTCTG TGTAAGAAAA CAACTNACAA	100
	AAAAGAAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC	150
40	NGGGGGAAAN TGCCNGGGC	169

		(2) INFORMATION FOR SEQ ID :235:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 51 base pairs	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
10			
10		(xi) SEQUENCE DESCRIPTION: SEQ ID :235:	
		GCANCACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA	50
15		G	51
		(2) INFORMATION FOR SEQ ID :236:	
	•	(i) SEQUENCE CHARACTERISTICS:	
20		(A) LENGTH: 101 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
25			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :236:	
70		CAAGTGTAAA TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC	50
30		TCAAACTTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA	100
		A	101
35		(2) INFORMATION FOR SEQ ID :237:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 156 base pairs	
		(B) TYPE: nucleic acid	
40	٠	(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	

G 50 A 100 C 150
C 150
156
T 50
A 100
148

GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA

	AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA	100
	AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA	150
5	TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG	200
	CCCTTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA	250
	TCTTCTCT	258
10	(2) INFORMATION FOR SEQ ID :240:	
	(i) SEQUENCE CHARACTERISTICS:	
*	(A) LENGTH: 377 base pairs	•
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :240:	
	GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA	50
25	CAAACCAGTG ATTCCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG	100
		•
	GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA	150
	·	
	CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT	200
30		
	TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG	250
	CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC	300
	CAGNIGCARC CAGNOGAGNI CCITINAAGN GNAACITOIN GNAITHIIMO	300
35	AAGGGTNAAC NTNTTTNNAA ANNNGCCNAA NCNNGATTTT GNACNCCCTT	350
33	ANGIGINALE WINITIWAL ANNAGERAL REMODITITI GRACUCCOTT	330
	MANAGE MANAGE AND	377
	TNNCATTGGC ATTNANTGAA AAAAGTT	37
	(A) TURBRUARTON POR CRO TR CAS	
	(2) INFORMATION FOR SEQ ID :241:	
40		
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 114 base pairs

•	(B) 11121 112121	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :241:	
•		
	GGNGCACTGN TCCGAGAGCT TTTTTTNCTG AAGAATAGCA TCTTTAATGA	50
10		
	GTGTNCTAAT CCTTGTCATC TGAAGTTTTG AAATATATTT CCCAGGGTCA	100
	GAACAATACA GAGA	114
15	(2) INFORMATION FOR SEQ ID :242:	
10	(2) Intolumiton for Dag to the	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 122 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(b) TOPOLOGI. Timear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :242:	
25	(X1) SEQUENCE DESCRIPTION. SEQ 15 .242.	
	CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTTNN CCATTAAAAA	50
	CTCAAAATNC TGTGACAAAT TINNNNGGTC AAGITGITAA COATTABBBB.	
	GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA	100
	GTACCTGATT TTCAAAAACC TAATAACCII AAAACCNCCC CACGNAAAAA	100
30		122
	AAAAANCNA AAGNGGGCCC CC	422
	242	
	(2) INFORMATION FOR SEQ ID :243:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 171 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :243:	
	GAGAATGGGA AGCCTCATTT TGGGGACAAG AACCTGTACA AGGATTTGTG	50
5	ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC	100
	NTATGATATG CCTCATGATA TINTIGCATC TGAAGATGGG ACTNTGTACA	150
10	TTGGNGATGC TCATCCAAAC C	171
10	(2) INFORMATION FOR SEQ ID :244:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 235 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :244:	
	AACTITACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT	50
25	TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAA GTTAAAACAG	100
	GACTTTCAAC TTAATCCAGA CTTCCTAACA GTGTTTACAT GTGAGGGAAA	150
	CTCCTTTAAG TAATGCGTAG TGTTTTATTT TTACCATCAT TGGNGACAAA	200
30	AAAAACAAAA ACATAAACAT CTNANGTGAA ATATA	235
	(2) INFORMATION FOR SEQ ID :245:	
35	(2) 200 200 200 202 20 200 200	
· - ·	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(XI) SEQUENCE DESCRIPTION. SEQ ID .245:	
	GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG	50
5	TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN	100
•	TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC	150
10	NTNTACNTCT AACCNTAACA TNACNGCGGC CACCTACTCA TGCCCTANTG	200
10	CAGCNCACCC T	211
	(2) INFORMATION FOR SEQ ID :246:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 194 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :246:	٠.
25	GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA	50
	AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT	100
30	ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT	150
30	GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA	194
	(2) INFORMATION FOR SEQ ID :247:	
35	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 249 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	·	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :247:	·
	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	.50
5	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	. 150
10	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
10	GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT	249
	(2) INFORMATION FOR SEQ ID :248:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 248 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :248:	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :248: GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
25		50
25	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	
	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	100
	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	100 150 200
30	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC	100 150 200
30	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC (2) INFORMATION FOR SEQ ID :249:	100 150 200
30	GCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC (2) INFORMATION FOR SEQ ID :249: (i) SEQUENCE CHARACTERISTICS:	100 150 200
30	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC (2) INFORMATION FOR SEQ ID :249: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 base pairs	100 150 200

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :249:	
	GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCGCGTTG	50
5	GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA	82
	(2) INFORMATION FOR SEQ ID :250:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 125 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :250:	
20	GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG	50
	TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN	100
25	GAGAGATGCA CAAGATTTAC AGGCC	125
	(2) INFORMATION FOR SEQ ID :251:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 130 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :251:	
	GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG	50
40	AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT	100

TCTGGGGGAG CGGCCGCCTT TAGTCGACCC

		(2) INFORMATION FOR SEQ ID :252:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 216 base pairs	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
•		(D) TOPOLOGY: linear	
	٠		
10		(xi) SEQUENCE DESCRIPTION: SEQ ID :252:	
		GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA	50
15		AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT	100
		TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT	150
		ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTTT	200
20		ATGNGATAAT ATCAGC	216
		(2) INFORMATION FOR SEQ ID :253:	
25		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 249 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
30			
		··	
		(xi) SEQUENCE DESCRIPTION: SEQ ID :253:	
35		GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAAATT	50
		ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTTCCTT CCAAAGAAGN	100
		TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA	150
40		TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT	200

TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT

. •	TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT	249
	(2) INFORMATION FOR SEQ ID :254:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 166 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :254:	
15	GACCCCATTC TATATTATNC GTNNNGCGAT TTTTTAGCCA CCCTGAAGTT	50
	ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG	100
20	GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG	150
	CTCCCTGGGN TTCTTG	166
	(2) INFORMATION FOR SEQ ID :255:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :255:	
35	CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG	50
	AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA	100
40	AGATTTGCTC GCTGAGAAAG TCCTTGTGGG AAATCGAAGT TGAGGACTAC	150
40	TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC	200

	CTTCTNTTGT NACAGACAGC AGA	223
	(2) INFORMATION FOR SEQ ID :256:	
5	(i) SEQUENCE CHARACTERISTICS:	
7	(A) LENGTH: 292 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :256:	
15	GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT	50
	TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCCGC	100
	TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA	150
20	CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC	200
	CTGACGATCT TTCCCTAGAT CATTCTGACC TGTTGTAGAG TTGTTGAAGG	250
25	AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC	292
	(2) INFORMATION FOR SEQ ID :257:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 238 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :257:	
	AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT	50
40	AND COMMON TO COMMON AND COMMON COMMO	100

	ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT	150
	GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA	200
5	TCTTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT	238
	(2) INFORMATION FOR SEQ ID :258:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 137 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	·
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :258:	
20	GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA	50
	GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG	100
	AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA	137
25	(2) INFORMATION FOR SEQ ID :259:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 241 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :259:	
33	(XI) SEQUENCE DESCRIPTION: SEQ ID :259:	
	GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC	50
40	TAGCCGGGAA GGGGCTCGGC TGGAGTGNNA AGGCTCAGAA AAATTTCGCG	100
	AAGAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT	150

.•	TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTTT CGTGTTACAT	200
	CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C	241
5	(2) INFORMATION FOR SEQ ID :260:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 248 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :260:	
	GCGGACTTTT AAGGGATTTG CNGTGATGCC TGTTGACCCA GTGCCTTCCT	50
20	AGCCGGGGAA GGGGCTCGGC TGGAGTGNNA AAGGCTCAGA AAAATTTGCG	100
20	AAGAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT	150
	TTTTGGACAG GTGGGGCGGT GACCTTGGTA TGTATTTTTC GTGTTACATC	200
25	GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA	248
	(2) INFORMATION FOR SEQ ID :261:	
•	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 239 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :261:	
40	GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA	50
40	CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT	100

	ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC	150
	ACTTCCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT	200
5	GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA	239
	(2) INFORMATION FOR SEQ ID :262:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 143 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
,		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :262:	
	GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTTTGTAA AACAGCCATT	50
20	GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG	100
	TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA	143
		240
25	(2) INFORMATION FOR SEQ ID :263:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 246 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :263:	
	GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC	50
4.5	TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC	100
40	TAAAAAAAA TAGCAATCCA GATAGGCTTC GATTTCCCGT GACACTCTGA	150
		150

	••	AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT	200
		TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG	246
5		(2) INFORMATION FOR SEQ ID :264:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 199 base pairs	
		(B) TYPE: nucleic acid	
10		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
15		(xi) SEQUENCE DESCRIPTION: SEQ ID :264:	
		GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT	50
20		CTGTGTTAAA TCGTATGCTT TTTAAAGGTA TTTAAAGATT CAACTAGCTT	100
20		TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG	150
		ACCTGATCTT GATGTTCTGC TGTTGTNAGT CTTGAAGAGC GTATNTGAT	199
25		(2) INFORMATION FOR SEQ ID :265:	
		(i) SEQUENCE CHARACTERISTICS:	•
		(A) LENGTH: 245 base pairs	
		(B) TYPE: nucleic acid	
30		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
35		(xi) SEQUENCE DESCRIPTION: SEQ ID :265:	
-		GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT	50
40.	٠	TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA	100
40 ,		**************************************	150

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	AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG	200
	AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG	245
·5	(2) INFORMATION FOR SEQ ID :266:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 121 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :266:	
	AGGAAAAGAT GGGAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG	50
20	TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTTNGC CTGCAATTCA	100
20	AGGCGAAAAT CCAAAGGCAT C	121
	(2) INFORMATION FOR SEQ ID :267:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 169 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :267:	
35	GGGTCGCTCT CCCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG	50
	TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCATC	100
40	TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC	150
40	AGGGTGGAGG CAGATGTCT	169

	••	(2) INFORMATION FOR SEQ ID :200.	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 200 base pairs	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
10			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :268:	
		TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG	50
			•
15		GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG	100
		CACTGCCAGC AGAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT	150
,			
		ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAACA AGTGCTGCCT	200
20			
		(2) INFORMATION FOR SEQ ID :269:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 163 base pairs	
25		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
30			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :269:	
		AGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG	50
35		ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC	100
		TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCT	150
٠.			
		CACTAAGTGT AGT	163
40			
		(2) INFORMATION FOR SEQ ID :270:	

.•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 115 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
· 5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :270:	•
10		
	TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG	50
	GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA	100
15		
15	CCACTTATTC TTTCT	115
	(2) INFORMATION FOR SEQ ID :271:	•
	(-)	
	(i) SEQUENCE CHARACTERISTICS:	-
20	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :271:	
	CCCCACACCOM CCCANNAMAC MAGMAMACA ACCAMACA ACCAMACA	
30	CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA	50
30	GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN	. 100
	GOGINITATO TIATOGOGGA CACTETACTA COGGATGCGT ATGATGNGGN	100
	NCCATTATNG NAGTGGGCAT TGGGGGGGAAA CAGAGCACCT GATGCTTTAC	150
		100
35	TGCAGAAATN CCTATGTGAC TCTTATAA	178
	(2) INFORMATION FOR SEQ ID :272:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

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(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :272:	
	CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA	50
	GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN	100
10	NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC	150
	TGCAGAAATN CCTATGTGAC TCTTATAA	178
15	(2) INFORMATION FOR SEQ ID :273:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 135 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :273:	
	CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACA	50
30	AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG	100
	CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC	135
	(2) INFORMATION FOR SEQ ID :274:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 231 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	·.
40		

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	131	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :274:	
	TGTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG	50
5	CTTGTCACAN GAAAGCACCA TGTTCGCAAT GGATTGCTGC AGGTGCTGCC	100
	GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA	. 150
	TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTTCCTTCAT	200
10	GACATAGGTG AGCAGTTTCC AGTCCCACTC C	231
	(2) INFORMATION FOR SEQ ID :275:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :275:	
25	TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC	50
	TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA	100
30	GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG	150
50	NCGTNCCCAC CATTGATTGA	170
	(2) INFORMATION FOR SEQ ID :276:	•
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid	
	CLI SIKANUEUNESSI OODDIE	

(D) TOPOLOGY: linear

	152	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :276:	
	ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA	50
. 5	ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG	100
	AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC	. 150
10	CTGAGGGAAA CTAATCTGGA TTCACTCCCT CTGGTTGATA CCCACTCAAA	200
10	AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA	250
_	ACGARACTIC TCAGCATTAC GATGACCTTG AATGARAATN GTACACACTT	300
15	AGCGTAGCAT ATTNA	315
	(2) INFORMATION FOR SEQ ID :277:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 209 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :277:	
30	ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTTGAGA TTTCACAAGC	50
	ARTGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC	100
	ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT	150
35	AGCAGAAATA GGCCCTTTCG TGNGCTGTTC TATTTNCTCG GATNGTAGAT	200
	ATAGTAATC	209
40	(2) INFORMATION FOR SEQ ID :278:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
J		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :278:	
	•	
10	AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC	5
10	TGCTGTTAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA	100
		10
	GAGTCTT	10
15	(2) INFORMATION FOR SEQ ID :279:	
	(1) INTOMITTON TON BEG ID .279:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 276 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	:
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :279:	
	AMCANCACAA AAGGAMGGMG GGAMGGMG	
	ATGAAGAGA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA	50
	CAGTGCAATA GGCTCCAAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT	100
30		
	ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG	150
	TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC	
	TAGGGAAAGC TCTCTCCATC	200
35	GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCCNCT ATAAGTGCAC	250
	AAAGGGGAAA CACTGATTTC AAGCTT	276
	(2) INFORMATION FOR SEQ ID :280:	
40		
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 185 base pairs

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	·	
· 5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :280:	
	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
10	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
15	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT	185
	(2) INFORMATION FOR SEQ ID :281:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :281:	
	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
30	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
35	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA	186
	(2) INFORMATION FOR SEQ ID :282:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 198 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5 .	(xi) SEQUENCE DESCRIPTION: SEQ ID :282:	
	TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTCGAGA GTCCATGTTC	50
10	TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT	100
	TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT	150
	GTAGGCACAG GGAGACTCAA AAGCACGAGT TNTGAAAGCG TAAATGGG	198
15	(2) INFORMATION FOR SEQ ID :283:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 222 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :283:	
	AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA	50
30	GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA	100
	CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC	150
	CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTTG ACAGCTTTCT	200
35	CAGCTCCCTG ACTCCGTTTA CC	222
	(2) INFORMATION FOR SEQ ID :284:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 162 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	·

(D) TOPOLOGY: linear

5		
5	(xi) SEQUENCE DESCRIPTION: SEQ ID :284:	
	ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA	5
		J
.10	ATGTGNGACG ACACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA	10
	CCTTTGNCGC TGTTTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG	15:
	TAGACTGCTT GG	13.
	Indicated in the second	16:
15	(2) INFORMATION FOR SEQ ID :285:	
	(i) SEQUENCE CHARACTERISTICS:	
	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 67 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(vi) SEQUENCE PROFILE	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :285:	
	GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA	
	. GAAGTTTTC TCCCGCGACA	50
	GACAGCAGAC TCGAGCC	
30		67
	(2) INFORMATION FOR SEQ ID :286:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 153 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	·	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :286:	
	E -D -200.	

	GGTCGGATCA GGTCACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA	50
	GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT	100
5	TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA	150
	GAA	153
10	(2) INFORMATION FOR SEQ ID :287:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 293 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :287:	
20	TACTACGGCT AAGGAGAAAC AATGTTCCTA CATATCACGG GTAGTGAGAA	
	THE THE CATATCACGG GTAGTGAGAA	50
	CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT	100
	The state of the s	100
25	CCATCGTGCT TTAGAAATAA CTGTATACAG TGTTATAAGT TGAAAAGAAC	150
	TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG	200
30	CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC	250
30	CATCOATCCC ATATANANCC CACATTONIA	
	GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC	293
	(2) INFORMATION FOR SEQ ID :288:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 114 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
4.0	·	

158

	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :288:	٠
	AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT	5
5 ,	CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC	10
	GTGTTGAATC ACTG	114
10	(2) INFORMATION FOR SEQ ID :289:	
10	(i) SEQUENCE CHARACTERIST	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 290 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :289:	
	ATGAACCAGT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTTGCTGGA	50
	AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC	100
25	CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC	150
	GCGGGCTGGG TCCCACCONA CTGCGCGAAG CTGCTGACTG AGGNGCACGC	200
30	AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT	250
	GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT	290
	(2) INFORMATION FOR SEQ ID :290:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 179 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double(D) TOPOLOGY: linear

• .•	(xi) SEQUENCE DESCRIPTION: SEQ ID :290:	
	AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN	50
5	NACTTIGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG	100
	TATCATNIGI GGCAGGACTI GNICCATATC AGIGITACII TIGCIACIGI	150
10	TTTGTAGAAC GATGTACATG AATGAGCCT	179
	(2) INFORMATION FOR SEQ ID :291:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :291:	
	TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG	50
25	TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT	100
	CTGTGGGATT CTGCCCAAGA GATCTCATTA CAGTTCCCAA TTCTTTGTTG	150
30	TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTTGAATC	199
	(2) INFORMATION FOR SEQ ID :292:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY, linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

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		•
	GGAAGACCAT TCTGATCATC CTCACTGACG CCAT GGCAA GAGGGTGGTT	50
	TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT	100
5	CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC	. 150
	AACCGAANNG ATATTACAAT GTAAAAA	177
	(2) INFORMATION FOR SEQ ID :293:	
10		
	(i) SEQUENCE CHARACTERISTICS:	
• .	(A) LENGTH: 295 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :293:	
20		
	ATTGGTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA	50
	CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC	100
		100
25	AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT	150
	TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACTTTGN GTCTGTTTCT	200
		200
	TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC	250
30	•	
	CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCGT	295
	(2) INFORMATION FOR SEQ ID :294:	
35		
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 78 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :294:	•
	AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG	50
·5	CATATTTTAC CATTTTGNAA ACTGTGAG	78
	(2) INFORMATION FOR SEQ ID :295:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 163 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :295:	
20	ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT	50
	GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG	100
	GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTTGAGA	150
25	GAGCCCGGTA ATA	163
	(2) INFORMATION FOR SEQ ID :296:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :296:	
	AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC	50
0 .		, 30
	CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA	100

	. TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT	150
	CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCTTC	189
5	(2) INFORMATION FOR SEQ ID :297:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :297:	•
	GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCTGTCCC CACTCACACA	50
20	AGTGGTCCGG TGTCACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT	100
20	GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG	150
	GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC	199
25	(2) INFORMATION FOR SEQ ID :298:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 181 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :298:	
	AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG	50
40	CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG	100
40	CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT	150

	GTATCATCAT GCTGCCTCCT GCATTTGAAT T	18:
	(2) INFORMATION FOR SEQ ID :299:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 314 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(with CROUDNER PROGRAPHICAL COLUMN	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :299:	
15	AACATTGTTT ATTCATCCAG CAGTGTTGCT CAGCTCCTAC CTCTGTGCCA	50
	GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTTAGC ACAGCCTGGG	100
20	GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA	150
	CTGCAAGCTG CTTGCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT	200
	CATCTGGTTG TGACTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT	250
25	TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC	300
	GAGGCATGTA CATT	314
30	(2) INFORMATION FOR SEQ ID :300:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :300:	
	AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC	50

	CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT	100
	TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA	150
5	AAGGAGAGAC AAGTGCAA	168
•	(2) INFORMATION FOR SEQ ID :301:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 142 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :301:	
20	ACCCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG	50
20	GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG	100
	CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT	142
- 25	(2) INFORMATION FOR SEQ ID :302:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 197 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :302:	
	AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT	50
	GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG	100
40	NOCCONDAN CONCRETENT TENETTETTA CTTCETTTCA CTCANGACAA	150

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	 TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG	197
	(2) INFORMATION FOR SEQ ID :303:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 236 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :303:	
15	AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT	50
	GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC	100
20	CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA	150
	TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT	200
	AAAAGTTTTT GAATAATGA TGAAAATTTT TTAACT	236
25	(2) INFORMATION FOR SEQ ID :304:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 220 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :304:	
	ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC	50
40	CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG	100
~~	TCTAGCACAG CCACCGCCC CATGCCCAGG CTCAGGAGCA CACTGAGGTC	150

	GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT	200
	TTAGGCCTCC CGTACAAACT	220
5	(2) INFORMATION FOR SEQ ID :305:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 145 base pairs	•
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :305:	
	AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA	50
20	ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAAGNTC	100
20	AACCTTCGAT GCTATCCCCC AGCCCAATAC AAAATCAGAA AAAGC	145
	(2) INFORMATION FOR SEQ ID :306:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 120 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :306:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID :308:	
35	AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT	50
-	TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG	100
40	NGNTGATATA AACAGATNNA	120
40	(2) INFORMATION FOR SEQ ID :307:	

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(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIN: 120 Dase pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	·	٠
	(xi) SEQUENCE DESCRIPTION: SEQ ID :307:	•
10		
	AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT	50
	MANAGEMENTS OF THE COMMAND AND ADDRESS AND	10/
•	TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG	100
15	NGNTGATATA AACAGATNNA	120
	NONTORIAL ARCAGAINNA	121
	(2) INFORMATION FOR SEQ ID :308:	
	<u>-</u>	
	(i) SEQUENCE CHARACTERISTICS:	
20 .	(A) LENGTH: 247 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
_		
25	•	
	(with growenon programment, and the 200.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :308:	•
	ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTTATCAT	50
30	ACTOCACOCA COCCARGOCC ATGCCAGGOT ATGCAGATGT CATTIATERS	٥,
	AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA	100
	GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC	150
35	TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG	200
•		
	AGCCGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG	. 241
	(2) INFORMATION FOR SEQ ID :309:	
40	(i) CECHENCE CUADACTERICATOR	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs	
	(u) prugiti, to, page hatta	

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	(with CEOURNOR DECORPORATION, CRO. TD. 200	-
	(xi) SEQUENCE DESCRIPTION: SEQ ID :309:	
	AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG	50
10		
	AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT	100
	ATGCGTT	107
		20,
15	(2) INFORMATION FOR SEQ ID :310:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 114 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :310:	
	() objected blockfillok. SEQ ID :SIU:	
	GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG	50
	ATTOTEGEET CONCECTORS CNOTENACIS NACIONAL CONTENACIONAL	
30	ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG	100
	TATCAGGAAA GAGA	114
	(2) INFORMATION FOR SEQ ID :311:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 237 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :311:	
	ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC	50
5	TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT	100
	TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC	150
10	GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA	200
10	GTTGTCATAA CCACCTCCGT AGCCCCCACC CTGTTGC	237
	(2) INFORMATION FOR SEQ ID :312:	•
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 147 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :312:	
25	TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG	50
	TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA	100
30	GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC	147
	(2) INFORMATION FOR SEQ ID :313:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 151 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		

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(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

•	CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG	50
	CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAAA	100
5	CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG	150
	G	151
••	(2) INFORMATION FOR SEQ ID :314:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 287 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :314:	
20	GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC	50
	AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA	100
25	AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT	150
	TATCACTAGG CTAAAACTGG ACAAAGACCG CAAAAAGATC CTCGAACGGA	200
30	AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA	250
	ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA	287
	(2) INFORMATION FOR SEQ ID :315:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 183 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :315:	
	GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT	50
5	GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTCCA	100
	CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT	150
10	GTAAACTAAG GTAGACTACT CTGNGAATAA GAA	183
10	(2) INFORMATION FOR SEQ ID :316:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 135 base pairs	
15	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :316:	
	GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTCAG AAAACGTGGG	50
25	TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG	100
٠	CCACCTTTGC AGCCTGTTTC TGTCATGTAG TTTCA	135
	(2) INFORMATION FOR SEQ ID :317:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 187 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
		•
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :317:	

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC

	TGCCGAAGTC CAAAAGCTTC AGCATTTCCT TAGTGTCAGG ATCTACTTCA	100
	ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC	150
5	CTATNTTTTC TGCGGCTTGA TGGAGATACC TTTACTG	187
	(2) INFORMATION FOR SEQ ID :318:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 268 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
3.5		
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :318:	
20	TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT	50
	GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT	100
	CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA	150
25	ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT	200
,	GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN	250
30	AGCTTTCNGT TGNNNTAA	268
	(2) INFORMATION FOR SEQ ID :319:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 138 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

	ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA	50
	AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA	100
5	GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT	138
	(2) INFORMATION FOR SEQ ID :320:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 118 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :320:	
	AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTTC ATAAACCTCA	. 50
20	GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT	100
	GTAATCATAC TTCCCCCA	118
25	(2) INFORMATION FOR SEQ ID :321:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 160 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :321:	
33	(XI) DEGOTION DEGOTITION DEG ID VOII.	
	AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG	50
· 40	GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC	: 100
	CTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT	150

	.•	TTCCTTTTCC	160
		(2) INFORMATION FOR SEQ ID :322:	
5		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 281 base pairs	
		(B) TYPE: nucleic acid	·
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
10			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :322:	
15		AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCCG	50
		AACAGGGCTG CTGATTGTTC CTTTCACTTT TGNGGTGACC TTGAGCTCCC	100
20		TTAAAAAAA AACTTGGAGA ATCACAACTG GCAATGCACC GCAGTTCTCG	150
		AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT	200
		GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA	250
25		ACCCCTGGG AGTATAATNN TCTCCATANA A	281
	•	(2) INFORMATION FOR SEQ ID :323:	
		(i) SEQUENCE CHARACTERISTICS:	
30		(A) LENGTH: 99 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
35			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :323:	
40		GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC	50
40		ANTITATION GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG	99

	(2) INFORMATION FOR SEQ ID :324:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 167 base pairs	
5 .	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10.		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :324:	
	GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC	5
15	ANTERTATION CONTROL AND CASE ACTOR CONTROL OF THE C	
10	ANTITATION GICTICITTA ANNIAGAGIG ACTIACIGAT ITATIATIGA	100
	CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA	150
	THE	13(
•	TTGCCCGCGT TTTTAGG	167
20		
	(2) INFORMATION FOR SEQ ID :325:	
	(i) SEQUENCE CHARACTERISTICS:	
o-	(A) LENGTH: 160 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :325:	
•	TGATCCAACT CTTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA	50
35	AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG	100
	ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCTCTT	150
10	TCGGGTCGCG	160
•0	(2) INFORMATION FOR SEO ID :326:	
	· (4) INFORMATION FOR DEG ID 1326:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :326:	
10		
	GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT	5
	GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG	10
15	AACATGAGAG AGCAGAGTGC TCTC	12
	(2) INFORMATION FOR SEQ ID :327:	
20	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 253 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(0, 000 00000	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :327:	
	AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA	
30	AGCCIAGITI GAACATCCIC ATCCCNGTGT TAGACCGGAT CCGATATACA	5(
	GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT	100
	CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA	150
2 =		
35	CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG	200
	CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACTCT CTCTGGACAA	250
•		25
	AGT	25
40		
	(2) INFORMATION FOR SEQ ID :328:	

177

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :328:	
10	GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA	50
	TAGAAGAAGC TCAGTATCGG CTCCTCCCAC CATAACCGCG TTNAAATCGC	100
15	CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCCATG CTCCTGCTAC	150
	CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT	200
	(2) INFORMATION FOR SEQ ID :329:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 280 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :329:	
30	TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC	50
	TCTTTCTTTT NTCGAAAATN ATAAAACTGC GTATTCTACT TTATATTTAA	100
35	TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG	150
	AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA	200
	TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA	250
40		•

GGATTACCAA CTCACTGCTG CCATGACCGA

(2) INFORMATION F	OR SE	Q ID	:330:
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	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 268 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :330:	
	(112)	
	CCTGAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT	50
15	CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA	100
	AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT	150
	Additional Column and	
	TCATATGTTC ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC	200
20	AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT	250
	CACTGCTGCC ATGACCGA	268
25	(2) INFORMATION FOR SEQ ID :331:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 170 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :331:	
	TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT	50
	AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN	100
40		

TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC

	TACCATATGC CCTTAAAAAT	170
	(2) INFORMATION FOR SEQ ID :332:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :332:	
15	TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT	50
	AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN	. 100
20	TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC	150
	TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGGTTCTGT	200
	GTTCCAAAAA TNTAAGATTT GTT	223
25	(2) INFORMATION FOR SEQ ID :333:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 132 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	\cdot	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :333:	
`	AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAACTCCCA CAAGTTCTTC	50
	TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG	100
40	TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC	132

(2) INFORMATION FOR SEQ ID :334:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 235 base pairs	
. 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
		•
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :334:	
	AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC	50
15	TGGAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT	100
	CCATNTTTGC CAATTTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNGCA	150
	\cdot .	
	GTAATGCCCT TGCTGCAGAC AACAACACCT GGACTGNGAG ATGGACCAAT	200
20	######################################	005
	TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT	235
	(2) INFORMATION FOR SEQ ID :335:	
	(2) INTOMMITTON TON DEG ID 1000.	•
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 169 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :335:	
35	ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC	50
	ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTCA TCAAGTTCGA	100
	CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG	150
40	avanga con nanconana	1.00
	GNGATCACCA ACAGGAGAG	169

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(2)	INFORMATION	FOR	SEQ	ID	:336:
(- 1	THIOMMITTON	1 011	222		

	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 193 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :336:	
	ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC	50
	TOTAL CONTROL OF THE PROPERTY	100
15	ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTCA TCAAGTTCGA	100
	CACHARANA CHICHOMANACC HEACHCACET CETAACCTAC CAACAATTGG	150
	CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG	130
	GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG	193
20	GROAT CACCH TIONS CHOICE CHOIC	
20	(2) INFORMATION FOR SEQ ID :337:	
	(2)	
	(i) SEQUENCE CHARACTERISTICS:	٠.
	(A) LENGTH: 307 base pairs	
25	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :337:	
		50
	CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC	50
25	TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA	100
35	TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA	100
	ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG	150
	WINCOIGING GOMMUNIOT TIGHTHING OTTOMOTHER GINGINGITIE	
	CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT	200

CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA

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	••	AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG	300
		CATCATG	307
. 5		(2) INFORMATION FOR SEQ ID :338:	٠.
10		 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		(xi) SEQUENCE DESCRIPTION: SEQ ID :338:	
		AAAAGTCATC CACAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT	50
20		CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA	100
20		TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC	150
		TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC	200
25		ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA	250
		AAGGCAAACT AAAACTGTCA TGCAGTGGTA GGTTTGAAAT NAGCTGCTGC	300
30		ATCAT	305
		(2) INFORMATION FOR SEQ ID :339:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 101 base pairs	
35	•	(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

	AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA	50
	ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG	100
· 5	G	101
٠	(2) INFORMATION FOR SEQ ID :340:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 113 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :340:	
20	GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGCGCA GGGGGCGTGG	50
	AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA	100
	AGGACTTCCC GCA	113
25	(2) INFORMATION FOR SEQ ID :341:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 209 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :341:	
	(x1) obgotnom procedition: SEQ ID :341:	
	ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT	50
40	ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC	100
	AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA	150

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•	ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA	200
	TTTCTAGGG	209
5	(2) INFORMATION FOR SEQ ID :342:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :342:	
	GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT	50
	TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA	100
20	GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT	150
	AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT	200
25	TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC	250
•	TA	252
30	(2) INFORMATION FOR SEQ ID :343:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :343:	

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT

	TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA	100
	GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT	150
5	AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT	200
	TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC	250
	TACAAAAC	258
10	(2) INFORMATION FOR SEQ ID :344:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 227 base pairs	
15	(B) TYPE: nucleic acid	
-	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :344:	
	GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC	50
25	CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG	100
•		150
	ATGACAAGGA TCACACCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA	150
		200
	TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG	200
30		227
	CACAGGACCC AGGAGTCCGC CCACCTG	227
	(2) INFORMATION FOR SEQ ID :345:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 188 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

• •	(xi) SEQUENCE DESCRIPTION: SEQ ID :345:	
	AAATAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG	50
5	TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC	100
	CTGGCACACT ACTAAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT	150
	CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA	188
10	(2) INFORMATION FOR SEQ ID :346:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 262 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :346:	
	AAATAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG	50
25	TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC	100
	CTGGCACACT ACTAAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT	150
20	CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT	200
30	NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC	250
	TAGAAGTGNA AA	262
35	(2) INFORMATION FOR SEQ ID :347:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 159 base pairs(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(XI) SEQUENCE DESCRIPTION: SEQ ID :347:	
5	CTCTGTTTTC CAAACGCCCA TGTGTGCTAT ACTACAACTC TTCTCGAGTC	50
	TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC	100
	ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTTAAAAGA	150
10	AATNTCTAA	159
	(2) INFORMATION FOR SEQ ID :348:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :348:	•
25	TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC	50
	ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT	100
	ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC	150
30	CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC	200
	TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA	250
35	TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC	283
-	(2) INFORMATION FOR SEQ ID :349:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :349:	
5	CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGGA	50
	CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC	100
10	GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG	150
	TGGATCACCC AGGTCAGGA	169
	(2) INFORMATION FOR SEQ ID :350:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 175 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :350:	
25	GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC	50
	AACCCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT	100
30	GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA	150
	CTTGGCAACA NCACAGGAAG GGACC	175
	(2) INFORMATION FOR SEQ ID :351:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 206 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
40	(D) TOPOLOGY: linear	

	189	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :351:	
	AAATAAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA	50
. 2	AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG	100
	GCACACTACT AACTGTAAAT GTTTTAAAAT TGAATCTGTA AAATTTGTAA	150
10	GGTTTTATGA ATATAATATT ATTAACTATT ATGTCTCTGA ATTTTTNNNN	200
	NAGGCT	206
	(2) INFORMATION FOR SEQ ID :352:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 76 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :352:	
25	AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG	50
	GACTTTAAAG CCGACAGTGA AATTAT	76
30	(2) INFORMATION FOR SEQ ID :353:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 245 base pairs(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40

ACATTTGGCC CTCAGACTGT AATTTCCATA CTACTNTGAC TGATACTAGA

	TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA	100
	ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG	150
5	GGCACTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC	200
	GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA	245
10	(2) INFORMATION FOR SEQ ID :354:	
10		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 179 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(5) Torossor. Timear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :354:	
20	GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC	50
	AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG	100
25	CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT	150
	CTTTGGGTTG AGACTTTTCA GNGACAACT	179
	(2) INFORMATION FOR SEQ ID :355:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	**
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :355:	

40

AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC

. •	TCCAGCATGT TGTCACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC	100
	AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG	139
5	(2) INFORMATION FOR SEQ ID :356:	· .
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 100 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :356:	
	TCCAGGAGAA GGAAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT	50
	GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT	100
20	(2) INFORMATION FOR SEQ ID :357:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 137 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :357:	
	AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGA AGACTAACCA	50
35 ·	AGATTTGGAC ATTGGAATGT TTACTGTTAT TCTTTAAGAA ACAACTACAA	100
	AAAGAAAATG TCAACAAATT TTTCCTAGCT AACTGAG	137
	(2) INFORMATION FOR SEQ ID :358:	
40		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 228 base pairs	

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(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :358: AAGGAACAAG TGGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG 50 10 ATCAGCTTGT CAATTTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT 100 TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAAACTGCA TCATGTCCCT 150 15 GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG 200 GGNACATGAG CAGCAGCTGN TCTTTAAC 228 (2) INFORMATION FOR SEQ ID :359: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 248 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double 25 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID :359: 30 CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT 50 CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA 100 35 CACTCACCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA 150 CCAAGAAAAT GAATAAAACA GCCAAACTCG ACCTTCTTAT GCAGAAAATT 200 GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC 248 40

(2) INFORMATION FOR SEQ ID :360:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 253 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :360:	
10	,	
	AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC	5
	CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC	10
15	TCTCTCTCCTCC CACACCCTC CAAAAAAAAAAAAAAA	
15	TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA	15
	CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT	20
		20
	GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT	25
20		
	GCC	25
	(2) INFORMATION FOR SEQ ID :361:	
	(2) Intermitted to N 329 ID :381:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 154 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :361:	
35	GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG	50
	GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT	100
	CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA	
40	TIME TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR	150
	TAAT	154

	(2) INFORMATION FOR SEQ ID :362:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(with groupher appropriately and the second	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :362:	
	GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG	50
15	GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT	100
	CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA	150
	TAATCCTGNC CACGCCCT	168
20		
	(2) INFORMATION FOR SEQ ID :363:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
25	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :363:	
	AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA	50
35	ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTC	100
	ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT	150
		150
40	CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT	198
	(2) INFORMATION FOR SEQ ID :364:	

	(I) SEQUENCE CHIMINATE INTERPRETATION .	
	(A) LENGTH: 121 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :364:	
	TTATACAAGT CAAACTTGGA AGGTCATAGT AAGCATACCT ATGCTGAGAG	50
,	AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC	100
15	TCGTACACTT TCAAGTTTAA A	121
	(2) INFORMATION FOR SEQ ID :365:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :365:	
30	GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA	50
	AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT	100
	TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC	150
35	GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT	200
	CTCCAAGGGA G	211
40	(2) INFORMATION FOR SEQ ID :366:	
-, 0	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 285 base pairs	

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear · 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :366: CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT 50 10 GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC 100 ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA 150 15 AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG 200 ATACAGTGGC CTTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT 250 TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG 285 20 (2) INFORMATION FOR SEO ID :367: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs 25 (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :: 367: GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG 50 35 GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA 100 ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT 149 (2) INFORMATION FOR SEQ ID :368: 40 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 base pairs

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
-		
5	·	
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :368:	
	GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG	50
10	CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG	100
	GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG	137
15	(2) INFORMATION FOR SEQ ID :369:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :369:	
	GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA	50
	CATGTAGTCC CTTTGTTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA	10
30	TAGAGTAAAT ATTGTTCCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA	150
	ATGTTAAACA NNNGTNAAAG TCTGTTTTGT CAATGCGGGA GT	19
35	(2) INFORMATION FOR SEQ ID :370:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 197 base pairs	-
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

•	(xi) SEQUENCE DESCRIPTION: SEQ ID :370:	
	GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTCGCCCACC AGCTCAGAGA	50
5	CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT	100
	GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT	150
10	ATAGTAGAAA CCAAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAAT	197
	(2) INFORMATION FOR SEQ ID :371:	
•	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 114 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20 ,		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :371:	
	GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC	50
25	ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC	100
	GGGCTTTGGA GAGG	114
30	(2) INFORMATION FOR SEQ ID :372:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 127 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :372:	
	CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG	50

	CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTTCTATG	100
	AACACGTTCT GCCTTTGCTG CTACTTC	127
5	(2) INFORMATION FOR SEQ ID :373:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 257 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	•
٠	(D) TOPOLOGY: linear	•
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :373:	
	AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC	50
20	TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCCTTA CTCAGTAGCA	100
	GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT	150
	TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG	200
25	CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT	250
	TTGGCAT	257
30	(2) INFORMATION FOR SEQ ID :374:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 180 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :374:	
40	COLUMN TO A CAMEGOOD A TO A TOTAL A COCTOCTO CAGAGGACTO	50

		NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT	100
		CCGTGGGAAT CACTGTCTGA GTCTTGTGTC TAGTATTGAC AGATATAGCT	150
5		TTGTTCTTGG AGTAGAATTA AGGAATTGCG	180
		(2) INFORMATION FOR SEC ID :375:	
10		 (i) SEQUENCE CHAR. TERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	٠	(B) 10102000 0	
		(xi) SEQUENCE DESCRIPTION: SEQ ID :375:	
		GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT	50
20		TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC	100
		TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT	150
25		TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAAC ATCTTACTGA	200
		TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG	250
		AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA	300
30		TTGATCAGAA AGCTGTGGAC TTA	323
		(2) INFORMATION FOR SEQ ID :376:	
35		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 223 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	

. •	(xi) SEQUENCE DESCRIPTION: SEQ ID :376:	
	GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG	5.0
. 5	AAATCACTCG CTGGTGTTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT	100
	ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG	. 150
10	ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG	200
10	AGTCAGTCCT GCATTTATGT CTT	223
	(2) INFORMATION FOR SEQ ID :377:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 122 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :377:	
25	GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC	50
	CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTTGTCAT	100
30	ATGGCTAATC AAGAGCCAGG TA	122
	(2) INFORMATION FOR SEQ ID :378:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 195 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

	GGCAGTGCGT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC	50
	TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCCTC	100
5	AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA	150
	AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT	195
10	(2) INFORMATION FOR SEQ ID :379:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 210 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :379:	
	GTAGCCCTGA GGTCATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG	50
	GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACTTG GAAGGTTATA	100
25	GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN	150
	GGTTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT	200
30	ATANNNNNGG	210
	(2) INFORMATION FOR SEQ ID :380:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

	CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT	50
	GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA	100
·5	ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA	150
	CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG	. 200
	GCCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA	238
10	(2) INFORMATION FOR SEQ ID :381:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 275 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :381:	
	GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA	50
25	ATAGCTGTTC ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT	100
	CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAACT	150
30	GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA	200
50	AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAAACAGG TGGAAGAAAA	250
	CCTAGCNCGC ACAGAACATA AGCTC	275
35	(2) INFORMATION FOR SEQ ID :382:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 96 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :382:	
	AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCCA ACACTTTAAA	50
5	CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA	96
	(2) INFORMATION FOR SEQ ID :383:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 196 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
,		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :383:	
20	GGACTTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA	50
	AGGAGCTCTG GGCACCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC	100
	TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT	150
25	CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG	196
	(2) INFORMATION FOR SEQ ID :384:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :384:	
40	AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC	5
	ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA	10

	CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG	150
	CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT	200
5	CCCCAT	206
	(2) INFORMATION FOR SEQ ID :385:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 134 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	*
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :385:	
	GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTCAC	50
20	CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG	100
	AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA	134
25	(2) INFORMATION FOR SEQ ID :386:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 161 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :386:	
	CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC	50
	ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA	100
40	CONCENCIOS NOCOCCACON ACANCECCAS TECNICACIAS GAGGAGGCGA	150

	GGACGAGGCG T	161
	(2) INFORMATION FOR SEQ ID :387:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESC TON: SEQ ID :387:	
15	GGTGAGCCTC CGCCATCCAG CF CAAAC TGTGG GAC CGCAGCTGTG	50
	CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGACAC TGAAAACACA	100
20	ACCAGTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGTT	150
	GTTTTTNAG GCAGTAATNT	170
	(2) INFORMATION FOR SEQ ID :388:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 250 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(2) 101020011 1111001	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :388:	
35	TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG	50
	GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA	100
40	GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAAC GGCTTCGGTT	150
40	TCTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC	200

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	ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTCA AACTGAAATC	250
	(2) INFORMATION FOR SEQ ID :389:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 268 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(b) ToroLogi. Timear	
20		-
	(xi) SEQUENCE DESCRIPTION: SEQ ID :389:	
15	GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT	50
	CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT	100
20	CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN	150
	TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG	200
	AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC	. 250
25	GTAGGGCNTG AGGGAGGT	268
	(2) INFORMATION FOR SEQ ID :390:	,
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :390:	
40	GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA	50
	GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT	100

•	TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG	150
	CCAGGTATAC ACCTTANAGA GGATGAC	177
5	(2) INFORMATION FOR SEQ ID :391:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	•
	(B) TYPE: nucleic acid	•
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :391:	
	GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA	50
20	TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG	. 100
	GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAAA	139
	(2) INFORMATION FOR SEQ ID :392:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 259 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :392:	
35	GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC	50
	TATCTGGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC	100
40	AGCCACCCTG GAGGAGAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA	150
	AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCCGAG	200

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	AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT	250
	GAGCCCAAT	259
5	(2) INFORMATION FOR SEQ ID :393:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :393:	
	AAAGATCATC AGTTTGGAAG GTACTGGTCC AATTTATCTA GGAAGTATCT	50
20	CTTGGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG	100
	CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG	150
	GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC	189
25	(2) INFORMATION FOR SEQ ID :394:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 97 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :394:	
	AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA	50
. 40	AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA	97
	(2) INFORMATION FOR SEC ID .305.	

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(A) LENGTH: 244 base pairs

	(xi) SEQUENCE DESCRIPTION: SEQ ID :395:	
10	AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTC	5
	GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC	10
15	CCCTTGACTG ATTTATTGTC GTCAAAAGCA TGTTCCTCTA TCTTTTNNNN	15
	TORGACGATO CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT	20
20	AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT	24
20	(2) INFORMATION FOR SEQ ID :396:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 185 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :396:	
	TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT	5
35	TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA	10
	GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA	15
40	TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG	18:
40	(2) INFORMATION FOR SEC. ID . 207	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
·5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :397:	
10	GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG	50
	CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG	100
15	AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC	150
	ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA	. 200
20	ACACTGCTTA TCTGACCC	218
20	(2) INFORMATION FOR SEQ ID :398:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 250 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) Torologi. Timear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :398:	
	GGAAGCAAAA AAACAAAACT AAGCTCGAAT TTGCTTCCAA ACCTGTAGAT	50
35	TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC	100
	CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT	150
40	GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTT GACCCCAGAA	200
	AACCCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGCCCAC	250

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	(2) INFORMATION FOR SEQ ID :399:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 278 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	·	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :399:	
	TCACTTGATT CATCCGTCGC GGGATTTGGG AGCACTAGCA ACATAATCAA	50
15	CACACTCCTA CAATCTTAGG CTTCACATGT GCTGATGATG ATGAAACCAA	100
		100
	CTCTGCCCCA ATCATCTCCC CTTCTNTTAG GGTCTTACTA CATATCGCAA	150
20	CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCACTACCC	200
20	TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA	250
	The state of the s	230
	ATAATGAGAT TAAATTTATG TTTCGAGT	278
25	(2) INFORMATION FOR SEQ ID :400:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 207 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :400:	
	(WI) DIED DIEDNITIENT BIG ID 1400.	
•	GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA	50
	GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA	100
40		
	GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTTA	150

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	TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA	200
	ATGTGTT	207
5	(2) INFORMATION FOR SEQ ID :401:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 217 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :401:	
	GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA	50
	GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC	100
20	AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC	. 150
	AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG	200
25	NTTCTCCAAA GATAGCC	217
	(2) INFORMATION FOR SEQ ID :402:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 225 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	·
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :402:	
	TTTACAATAG ATTTCACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT	50
40	CTTCCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC	100

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	CAATTATCTT CTCGACAGCA TATACAGAAT CCCCACATCT GGAACACTTC	. 150
	TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA	200.
5	GGCCTGTGAG GCTGAACACT CTCTG	225
	(2) INFORMATION FOR SEQ ID :403:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :403:	
20	AGAAGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG	50
20	ACTGNGGCTT CCACTGCGCC CGTGTACNTT ATCGAAGCTA CAGAT	95
	(2) INFORMATION FOR SEQ ID :404:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 239 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :404:	
35	AGGAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG	50
	CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG	100
. 40	GGCCACACTG TGTAATACTG TGCCAACTTA TGCGAGTCTC ATTGTTCAGG	150
40	The second of th	200

	CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG	239
	(2) INFORMATION FOR SEQ ID :405:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :405:	
15	GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA	50
	TGTTCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG	100
20	AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA	150
	GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC	189
	(2) INFORMATION FOR SEQ ID :406:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 75 base pairs	
	. (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :406:	
35	CACCATCCTC CAAGTAAATC CCCCCTTAGG AAAGTAAGGG AAAAGACCCC	50
	TTATAGCCCT GAGCTCCCCC TTGGA	75
40	(2) INFORMATION FOR SEQ ID :407:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 190 base pairs	

	(B) TIPE. Macteta data	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5	·	
J	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :407:	
	TATTCATCCA GCAGTGTTGC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT	50
10		
	TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT	100
	CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG	150
15	CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC	190
	(2) INFORMATION FOR SEQ ID :408:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 194 base pairs	
. 20	(B) TYPE: nucleic acid	
	· •	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :408:	
	GAAGACATGG CGCCCTAACA CTTCGAGACC TGCTGNTAAA TTAAAAGCTA	50
30	·	
	TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG	100
•	CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG	150
35	CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT	. 194
	(2) INFORMATION FOR SEQ ID :409:	÷
	(2) INFORMATION FOR SEQ ID .403.	
	// CDOUDNOD OUNDACEDICATOR-	
4	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 97 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :409:	
	GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATTA TAACCACTTC	50
10	TAAAACAAGA TCATCTTCTG CAGCACCTGG TTTTAGTTTA TCCTTGA	97
	(2) INFORMATION FOR SEQ ID :410:	•
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 155 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :410:	•
	TTTGAGCTCC TGGACCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG	50
25	ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTTNTG GTCCAGGGCC	100
	AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC	150
	TTTGC	155
30	(2) INFORMATION FOR SEQ ID :411:	
	(i) CROURNOR CUNDACEMENTOR	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 249 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

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	AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA	50
	AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC	100
. 5	TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG	150
	TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA	200
	TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT	249
10	(2) INFORMATION FOR SEQ ID :412:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 143 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :412:	
	(XI) DEQUENCE DESCRIPTION. DEQ 15 .412.	
	AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC	50
25	TTTACTCCTC TATAACTCAT CTTCACACCN GCATATTTAA ACAAACTAAC	100
	AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT	143
	(2) INFORMATION FOR SEQ ID :413:	
30		
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	·	

GGGTCCCCC ATTCACGTAC TCCATCACAA AGTACAGGCG GTCCATGGTC

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	TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA	100
	CACCCACTTC TCCACCATAG TGCACTCCAC GTCATCATCT GATCACAACG	150
5	TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT	200
	GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT	250
	AAAATC	256
10	(2) INFORMATION FOR SEQ ID :414:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 87 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :414:	
	TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA	50
	TOGORARAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA	50
25	GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC	87
	(2) INFORMATION FOR SEQ ID :415:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 247 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :415:	
40	AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT	50
40	TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCGCCCGC	100

••	GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC	150
	ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG	200
5	CAGTGTTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC	247
	(2) INFORMATION FOR SEQ ID :416:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 162 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
. 13		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :416:	
	TCTAGCACAC AGCTGCGCTC ACAAAAACTG CGCGACTTGT TAGAACTAAT	50
20	TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA	100
	TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATTT	150
25	ACATTGAAAG GA	162
	(2) INFORMATION FOR SEQ ID :417:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 109 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) 101010011 1111111	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :417:	
	CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTTAA	50
40	GTACTTAGCA AAATATTTGT TTTNCGTGAT TTAGCTTGTC ATTAAACNAA	100

	GAGCTACTG	109
	(2) INFORMATION FOR SEQ ID :418:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 202 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :418:	
15	GGATGTAAAT TATATGTTGT TTAAATTTTT CCAGCATCTG AAAACCTTAT	50
	CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTTT	100
20	TAAATAGTAC ATATCATTAA ACCATTCNTT CTAAANGTAA GAAGAGCAGA	150
	AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA	200
	AA	202
25	(2) INFORMATION FOR SEQ ID :419:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 152 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(with Gravenar property and the	
. .	(xi) SEQUENCE DESCRIPTION: SEQ ID :419:	
	TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC	50
40	ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG	100
	CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTACCC	150

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		(2) INFORMATION FOR SEQ ID :420:	
5		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 218 base pairs (B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	•
		(D) TOPOLOGY: linear	
10			•
	•	(xi) SEQUENCE DESCRIPTION: SEQ ID :420:	
15		CAGCCCTACA CTCGCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA	50
		TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA	100
20		AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTTGG	150
20		CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT	200
		CTGCAATGTA GGGGCCGG	218
25		(2) INFORMATION FOR SEQ ID :421:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 237 base pairs	
30		(B) TYPE: nucleic acid	
30		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
35		(xi) SEQUENCE DESCRIPTION: SEQ ID :421:	
		GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAAACT CCCCCACCCA	. 50
40		GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC	100
40		CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC	150

	TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC	200
	ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA	237
5	(2) INFORMATION FOR SEQ ID :422:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 202 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15 .	(xi) SEQUENCE DESCRIPTION: SEQ ID :422:	
	AGGNGTAATA AATACTGCAT CCTTTCCACA ACATAGCAGG AATCTTATAG	50
20	GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG	100
	TTTCTTTACG AAGTGTAAAT AAGTGCTGCA CCATACTGTA AACAAAACTC	150
	GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT	200
25	cc	202
	(2) INFORMATION FOR SEQ ID :423:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 216 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :423:	
40	GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG	50
	AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA	100

	TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAAT	150
	ACTGACTTCG GTTTCTTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA	200
. 2	TTCGTATCAG CACCTA	216
	(2) INFORMATION FOR SEQ ID :424:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :424:	
20	CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT	50
	GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC	100
	CCATACCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG	150
25	GGTGCCCTTT TAAAAAAA	168
	(2) INFORMATION FOR SEQ ID :425:	
•	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 258 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :425:	
40	TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC	50
	TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTCA	100

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••	GAGGAGTCAC AGTGGAACTT CCCAGCTTTA AGATATCTAG CAGAAACTAT	150
	AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG	200
5 .	GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC	250
	TAATTAGG	258
	(2) INFORMATION FOR SEQ ID :426:	
10	() CROUDNOR GUARAGMERICATOO	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 275 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
13	(b) 10102001. 11hear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :426:	
20		
	TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG	50
	CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN	100
25	GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC	150
	CATGCACGAA GGACTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG	200
	CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTTGTGCC AGCTGCTGTT	250
30	CGAATNNTTT TCTTTCTCGT AAAGC	275
	(2) INFORMATION FOR SEQ ID :427:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 162 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :427:	
	CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA	50
5	GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTTNTGGC AAACTGTCGG	100
	GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT	150
10	CTAAGAGTGC TC	162
10	(2) INFORMATION FOR SEQ ID :428:	
	(i) SEQUENCE CHARACTER_STICS:	
	(A) LENGTH: 220 base pairs	
15	(B) TYPE: nucleic acid	
	. (C) STRANDEDNESS: double	
	(D) TOPOLOC:: linear	
20		
,	(xi) SEQUENCE DESCRIPTION: SEQ ID :428:	
	ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC	50
25	CCATAGTTCC TGAACTCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC	100
	·	
	TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA	150
	GTCGNGTTTA CAATGATTTG NCCTGGACTG AAATTCANGC TGCCTTAAGG	200
30		
	TGCTGATGAT ATTGAGAAGT	220
	(2) INFORMATION FOR SEQ ID :429:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 185 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

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. •	(xi) SEQUENCE DESCRIPTION: SEQ ID :429:	
	GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA	5(
5	GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT	100
	GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG	150
10	GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA	185
	(2) INFORMATION FOR SEQ ID :430:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 277 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	. •
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :430:	
	GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC	50
25	TACCTGGTCG TGGGAGTAGT GGTCATCGTG GACCCAGGGG TGATCCCTAT	100
	CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC	150
30	TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG	200
	GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG	250
	GAAGACACCG CAGAGCTCAC TTACCAA	277
35	(2) INFORMATION FOR SEQ ID :431:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs	
	(A) LENGTH: 125 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :431:	
5	AAAGTGCGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGCGCTGGTC	50
	GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT	100
	CAGCAAGGAG GAAGAAGTCA TTGTT	125
10	(2) INFORMATION FOR SEQ ID :432:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 222 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :432:	
	GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT	50
25	TCGAAATAGC ACATTTTTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA	100
	GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC	150
	AATTCCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT	200
30	ANAANGGAAA TGGGGCAGGA CA	222
	(2) INFORMATION FOR SEQ ID :433:	
	(i) SEQUENCE CHARACTERISTICS:	•
35	(A) LENGTH: 213 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

••	CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT	50
	CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC	100
· _. 5	CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT	150
ì	TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT	200
	NGNCGTTTCC TCT	213
10	(2) INFORMATION FOR SEQ ID :434:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 221 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :434:	
	CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT	50
2 5	CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC	100
	CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT	150
20	TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT	200
30	NGNCGTTTCC TCTGCCGGTG T	221
	(2) INFORMATION FOR SEQ ID :435:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 70 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :435:	
	ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT	50
5	TAGTATATTT TCGTTGTCAG	70
;	(2) INFORMATION FOR SEQ ID :436:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 163 base pairs	
	(B) TYPE: nucleic acid	
·	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :436:	
	AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT	50
20	CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA	100
	GACTGATTGA GTACAAAATG AAACTGTGCG TCAGCTTGAT CCATTTTGTC	150
25	ACCCTCAAGT AGG	163
	(2) INFORMATION FOR SEQ ID :437:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 170 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :437:	
	TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA	50
40	AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA	100

	AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG	150
	CTCAGCAACC CCTGAATTTG	170
· , 5	(2) INFORMATION FOR SEQ ID :438:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 187 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :438:	
	AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG	50
	AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA	100
20	GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAACTGTGT	150
	AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA	187
25	(2) INFORMATION FOR SEQ ID :439:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 234 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :439:	
	AAAAGCAACC AGGTTCGAGA AACAATAGTG TATGTGTTCC TATAGGTATG	50
	AGTTATTCAN TGTAGATTCG TTTTTCTGCA ATCCTCTGCC GAAATGATNT	100
40		157

	TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA	200
	CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT	234
5	(2) INFORMATION FOR SEQ ID :440:	
	(i) SEQUENCE CHARACTERISTICS:	
ř	(A) LENGTH: 203 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	· ·	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :440:	
	GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTTCCAGTT GACACCAAGT	50
20	CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA	100
	CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA	150
	ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG	200
25	TTC	203
	(2) INFORMATION FOR SEQ ID :441:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 254 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :441:	
	GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC	50
40	TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA	100

. •	ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT	150
	GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT	200
, 5	TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT	250
,	GGTT	254
	(2) INFORMATION FOR SEQ ID :442:	
10		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 147 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :442:	
20	GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG	50
	CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG	100
³ 25	CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC	147
	(2) INFORMATION FOR SEQ ID :443:	
	A CONTRACT OUR DROWNING CONTRACTOR	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 198 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) 10100001. 11.1001	
35		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :443:	
	GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG	50
40		
	CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG	100

	CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC	150
	TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT	198
_, 5	(2) INFORMATION FOR SEQ ID :444:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 208 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :444:	
	ATACTACGCT AGGAGAACAA TGTTCCTACA TATTATGGGT AGTGAGACAT	50
20	TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTCA	100
20	TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA	150
	AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT	200
25	TTCTGTGA	208
	(2) INFORMATION FOR SEQ ID :445:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :445:	
	AGCACATTTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT	50
40	CACTETTETE TECAGETTES CENTTEETEN TICETTEES SECTECETS	100

	TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA	150
	CCTGNAGCCC CCGCTGAG	168
, 5	(2) INFORMATION FOR SEQ ID :446:	
	(i) SEQUENCE CHARACTERISTICS:	
i	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleic acid	-
10	(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :446:	
		50
	AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCTGATT GGTGGATAAA	50
•		100
	GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA	100
20	THE THE COMMON CONC. STEECECTCA	150
	TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA	
	AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA	200
•	AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTCATO	
25	CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA	243
	(2) INFORMATION FOR SEQ ID :447:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 251 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) 1010D011 ==	
35		
33		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :447:	
	TO THE TOTAL TO THE CONTROL OF CTCTTTAGA	50
	CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCCAC CTGTTTTAGA	
40	AATCTAAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTTTAGAC	100
	AATCTAAAAT NNTAAGTAAC TAAGAGCAAA GIGCIAIGIG GELLE	

CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GGTGCTCTGG	200
5 GGAGGAGAG GGAGAGAAAA GGCTGTTTTG GAAAATATCC AGCACTTTGA	250
, c	. 251
(2) INFORMATION FOR SEQ ID :448:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs	
(B) TYPE: nucleic acid	٠.
(C) STRANDEDNESS: double	
15 (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID :448:	
20 ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNGCAGGA ACGTGATGGC	50
AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT	100
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTTAGAT	150
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA	200
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA	250
30	. 253
GTG	
(2) INFORMATION FOR SEQ ID :449:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·

_	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :449:	
	ATATAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA	50 -
_. 5	ATACCTCTGT AAGAAGCAGA ATACACCATA TGTTATTCAC ATGTATAGGA	100
	GTGATAAGAA AAT	113
	(2) INFORMATION FOR SEQ ID :450:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :450:	
20	TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA	50
	GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA	100
25	AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG	150
-	AAACTATTTG AGATCAAAGT CCTATAAACA AAGTTAAATG ATTCCAAGAG	200
	GTAAATAGGA G	21
30	(2) INFORMATION FOR SEQ ID :451:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 194 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(n) mororogy: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

. •	CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG	50
•	NATITCACAC NIGNCAGAGC TATAAACCGG IGNAIGAIGI GATITINCIG	100
		150
5	TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTTCAAGCA	
;	GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG	194
•	(2) INFORMATION FOR SEQ ID :452:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :452:	
20	ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA	50
	TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT	100
25	TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA	150
	CTATAGTGAT GCTTGCAA	168
•	CTATAGTGA1 GC11Gcim.	
	(2) INFORMATION FOR SEQ ID :453:	
30	(i) SEQUENCE CHARACTERISTICS:	:
	(A) LENGTH: 220 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :453:	
40	CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCCAGAC GTGAACCAAT	50

٠	TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCTTCAC	100
	TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA	150
5	TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA	200
	TAGGACGCCA GACTACACTG	220
10	(2) INFORMATION FOR SEQ ID :454:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 275 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	\ -,	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :454:	
20		
	GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA	50
	AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT	100
•		•
[.] 25	TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT	150
	ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTCAA	200
	ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA	250
30		075
	TAGTTTTGCT TTGTCTTTAG CGGTT	275
	(2) INFORMATION FOR SEQ ID :455:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 270 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	:455:
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	(WE) DEPONDED DEPONITION: SEQ ID :455:	
	TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA	50
5	ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG	. 100
	CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGACTTCCTT	150
10	AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTTG	200
	TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA	250
	TGCTCTNGGG TCTGCCCATT	270
15	(2) INFORMATION FOR SEQ ID :456:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :456:	
	TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC	50
30	ACGACCCCTG CGCTGGATAC GGCGACGGTT TCTCATTTCG CCTTTGCCAG	100
	CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT	150
	TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTTGTAGC CTTCAACTTA	200
35	TTTAAACTAC CAAGGAAGTT CAGGAACTTC CTCAANACGA TGACCTTTAG	250
	ACAT	254

(2) INFORMATION FOR SEQ ID :457:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

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241

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
_		
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :457:	
10	ACACTAACTG TTCCATCCGT TATATTTGCT GTGAGGAAAA TTAAGATTCC	50
	TGTTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG	100
	TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACA AACCAAGAGA	150
15	GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG	200
	TTTCCCCAAT GACTGTAATT TATAAACTAA AAATTG	236
20	(2) INFORMATION FOR SEQ ID :458:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 108 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :458:	
30	GAGANNNNTT NNGGNAAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG	50
	NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC	100
35	GCTGGTAT	108
	(2) INFORMATION FOR SEQ ID :459:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 155 base pairs	
	(B) TYPE: nucleic acid	
	· · · · · · · · · · · · · · · · · · ·	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :459:	
	ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC	50
10	CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC	100
10 .	CCATGTTCCT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA	. 150
	GAGGT	155
15	(2) INFORMATION FOR SEQ ID :460:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :460:	
	TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC	50
30	CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT	100
	CTGGTTTGTG GAGGTTCACA GACATGTGTT AGTATATCCT TGCCTGCATG	150
	TAGTTGTTCA TTACTAGAC	169
35	(2) INFORMATION FOR SEQ ID :461:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 184 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :461:	
5	ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT	50
5	CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT	100
	TTTATCAGCG TACCTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG	150
10	GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT	184
	(2) INFORMATION FOR SEQ ID :462:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 275 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :462:	
25	AGGAACCNTG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT	50
	TACTCAGTGC TUNCAGGCTG TGAGTUAATA GAGUGTGTAT GACTTAATAA	100
	GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA	150
30	GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN	200
	AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT	250
35	NNACTGNGTT GTTGGCGACA GATGT	275
	(2) INFORMATION FOR SEQ ID :463:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 149 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :463:	
. 5	AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA	50
	ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT	100
10	GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA	149
10	(2) INFORMATION FOR SEQ ID :464;	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 179 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
÷	(b) TopoLogi: Tinear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :464:	
	ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT	50
25	CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT	100
	GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG	150
	CCCAAGTCAC ACAGCTAGTG AAGACCAGA	179
30	(2) INFORMATION FOR SEQ ID :465:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 156 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID :465:

	CTACCTCTGT GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC	50
	TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA	100
, · 5	GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA	150
ř	CCAGAG	156
10	(2) INFORMATION FOR SEQ ID :466:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :466:	
	ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA	50
•	CTGCTGGTTC TGGTTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC	100
³ 25	TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGGCCTCACC	150
	ACTCCCCTNT GTCCCCCCAG CAGGGGGACA AAACAG	186
30	(2) INFORMATION FOR SEQ ID :467:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 87 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
3 5	(D) TOPOLOGY: linear	
	(wi) CEOURNAL PROGRESS CO. C. C.	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :467: TNNNGATGAN TATANAAGCA TCATNGACGG TATTTCCCNG TCTTGNANTT	
	TATALOGICAN TATALOGACIO TEATROCCONO TEATRO	50

	TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT	87
	(2) INFORMATION FOR SEQ ID :468:	
5	(i) SEQUENCE CHARACTERISTICS:	
-	(A) LENGTH: 187 base pairs	
,	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	ī
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :468:	
15	ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA	50
	TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTTGTTGG	100
20	AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT	150
	AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA	187
	(2) INFORMATION FOR SEQ ID :469:	
¹ 25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 256 base pairs	•
	. (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :469:	
35	AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA	50
	GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT	100
40	GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA	150
	ACATCGCCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA	200

	GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA	250
	ACTGAA	256
5	(2) INFORMATION FOR SEQ ID :470:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 109 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :470:	
	CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT	50
20	GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA	100
20	GAGGGTTTG	109
	(2) INFORMATION FOR SEQ ID :471:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :471:	
35	GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAAACTTT ATCAATCATA	50
	GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT	100
40	ATATATAT CCTACAGGCT GAGAAAGCTT TGNATTTCT	139.
	(2) INFORMATION FOR SEQ ID :472:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
•		
		•
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :472:	
10		
	TCGCAGGAGA AGGAATGTTC CCAATAGGAA CGCCTGTAGA CTGTTCAGAA	5
1	GARATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG	10
	GARATGCCCA RATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG	10
15	GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGA CTATTAACGG	15
	CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTCACGT	20
	GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA	25
20		
	TGGGAGACAT TT	26
	(2) INFORMATION FOR SEQ ID :473:	
	(2) INFORMATION FOR SEQ ID .473.	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	·
30	(D) TOPOLOGY: linear	
30		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :473:	
35	ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC	F
	ACAGAAGGAC TITGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC	5
	GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT	10
	·	
40	GCATCTCTCA TACTINNTAC AGCCAACATG AACACTCTAT GTATTTTCTA	150
40	AGCTTTCNTC TGTTCAAGAA CTTTGAATTT AAAACGTCT	18
	respectively of the termination	10

(2) INFORMATION FOR SEQ ID :474:

5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 166 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
	re_ `	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :474:	
	TNCGTGCCTA GCAAACTTAA ACTCGAACGC ACGTAATAGT GCTCATAATT	50
15	CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGACTCTAGC	100
	AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT	150
20	GTTAGTACGC GNGTTA	166
•	(2) INFORMATION FOR SEQ ID :475:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 109 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
`	(xi) SEQUENCE DESCRIPTION: SEQ ID :475:	
	TTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT	50
35	TCCTTCAAAA CTGTGTTTTG ACCACACAG GTGGGCATTA ACAAACAAAT	100
	TCAACTTAA .	109
40	(2) INFORMATION FOR SEQ ID :476:	
40	(i) SEQUENCE CHARACTERISTICS:	
,	(A) LENGTH: 131 base pairs	
	() mought for page hairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :476:	
	TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA	50
10	GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA	100
•	CGGGTCACTC AGTTACGTTT AGCCACAGCC T	133
15	(2) INFORMATION FOR SEQ ID :477:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :477:	
	ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCCTAC	50
30	ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT	100
	TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC	150
	AGTGTTATAA GTTGAAAAGA ACTCAAAATA ACTAATACAA ATATACACTA	200
35	CGTATTAGAA TTCAAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT	250
	AAAAAGACA CAAAT	265
40	(2) INFORMATION FOR SEQ ID :478:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) IENCTH. 182 baco pairs	

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251

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) TOPOLOGI: Timear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :478:	
10	AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAAGACC	50
	TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTTGT	100
	ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT	150
15	NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG	182
	(2) INFORMATION FOR SEQ ID :479:	
•	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 169 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
0.5		
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :479:	
30	AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA	50
	CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA	100
	AACGGGAGCC TCTAAATCTT GGTCGGGACT GCTCGCCTGG AGCCGCACTC	150
35	TTGAGTCCGA GGCCATCTT	169
	(2) INFORMATION FOR SEQ ID :480:	· .
40 ·	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 238 bas pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :480:	
	AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT	50
10	CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTTCTGTC TCACCGGATA	100
10	TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT	150
·	GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA	200
15	ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC	238
	(2) INFORMATION FOR SEQ ID :481:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 201 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :481:	
30	TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC	50
	TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCGAA GTCTGCAAGC	100
	AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG	150
35	ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG	200
	C	201
40	(2) INFORMATION FOR SEQ ID :482:	
	(i) SEOUENCE CHARACTERISTICS:	

(A) LENGTH: 162 base pairs

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253

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
3		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :482:	
	CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
10	CONTINUE TOTTOGGGG ANGHONOTOT ANGGGAAAAT TGGAAAACTC	50
	CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
	CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
15	ACNTTTTTAG AT	162
	(2) INFORMATION FOR SEQ ID :483:	
	•	
20	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 250 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) Toroboot. Timedi	
25		
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :483:	
	(110)	
	ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
30	ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
		100
	AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACTCNT NCCTGAACCT	150
35	GAGGGAAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
	CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAAACT	250
	(2) INFORMATION FOR SEQ ID :484:	
40		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 132 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	,
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :484:	
10	AACATTATCT TGACAAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG	50
10	AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG	100
	ATTAGAATGT TAATGCCACT TTGATTAGAT CT	132
15	(2) INFORMATION FOR SEQ ID :485:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 129 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :485:	
	TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC	50
20	CGCATTCACG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC	100
30	ACGGACTTCT CGACACCATC AAGAGCGAC	129
	(2) INFORMATION FOR SEQ ID :486:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
-	(D) TOPOLOGY: linear	
40		

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	(X1) SEQUENCE DESCRIPTION: SEQ ID :400:	
	TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG	50
5	AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG	100
;	ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT	150
	CATTGCACTT CAACCATATC GA	172
10	(2) INFORMATION FOR SEQ ID :487:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	•
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :487:	
	ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA	50
25	TTTAAAAGGC GACCACCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA	100
	TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC	150
30	AGCACTCCTC TATGGGCACA GACACACA CAAAATTGTC CTTGCTTTTC	200
	TCAGATATAT	210
	(2) INFORMATION FOR SEQ ID :488:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 90 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :488:	
	(111, 112, 111, 111, 111, 111, 111, 111,	
	ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC	50
5	ANACGTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT	90
	(2) INFORMATION FOR SEQ ID :489:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 99 base pairs	
,10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :489:	
	ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA	50
	TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC	99
	(2) INFORMATION FOR SEQ ID :490:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :490:	
35	GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG	50
	CCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC	100
	TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA	150
40	GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCCGA	186

	(2) INFORMATION FOR SEQ ID :491:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 263 base pairs	
5	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	. •••	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :491:	
	AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA	50
15	ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT	100
٠.	TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT	150
20	GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG	200
	CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC	250
•	TTCATATCGG AAA	263
25	(2) INFORMATION FOR SEQ ID :492:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 159 base pairs	
	(B) TYPE: nucleic acid	•
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :492:	
	AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT	50
40	AAATNGGTGT GGGNGGTCCG CTTTTGGCCA TCATCGCACC CCCCCGGTCA	100

CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA

	.•	CCGTGGGTC	159
		(2) INFORMATION FOR SEQ ID :493:	
, 5		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 197 base pairs	
;		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
10			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :493:	
15		GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGGTA	50
		CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT	100
20		CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA	150
		AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT	197
		(2) INFORMATION FOR SEQ ID :494:	
25		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 188 base pairs	
		(B) TYPE: nucleic acid	
•		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
30			
•			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :494:	•
35		GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA	50
		GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC	100
40		CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG	150
		CONCOCOMOC MEMONEMECON EMEMORIAN CEMENETA	188

	(2) INFORMATION FOR SEQ ID :495:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 169 base pairs	
, 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
,	(D) TOPOLOGY: linear	•
,	e_	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :495:	
	ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG	50
15	GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTTGCCACG AGAGTGAGAC	100
	GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT	150
	GTGGGNGCTG CTGGGGAGG	169
20	(2) INFORMATION FOR SEQ ID :496:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :496:	
	CAGAGAGAAC GTTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG	50
35	AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAGTCCC	100
	ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC	150
	TTTAAACCGT CAAGCTGGGT GG	172
40	(2) INFORMATION FOR SEC ID .497.	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 246 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
.5	(D) TOPOLOGY: linear	
•		•
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :497:	
10	GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG	50
	TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCGGTC	100
15	ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA	150
	ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCCACCCC TTAGGGTGTG	200
	TNTCATCGAA GTGTAGNGAA TGGTGGAACG TTTGTTTGTN GTGTGC	246
20	(2) INFORMATION FOR SEQ ID :498:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 215 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
		•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :498:	
	GCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT	50
	\cdot	
35	CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG	100
	CCACTATTTT TGTTGTATAT CTTCATCTCA ATGGCGACAT GGCCACTGCC	150
	CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT	200
40		015
	GAACATCGTG CGTTA	215

150

200

250

	(2) INFORMATION FOR SEQ ID :499:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 195 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	#_	
10	A CONTRACT PROGRAMMENT OF ACC.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :499:	
	GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT	50
15	AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC	100
	ACANGAAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG	150
	GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT	195
20	(2) INFORMATION FOR SEQ ID :500:	
	() CTOURNOR CUNDICATEDICATION	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs	
25	(B) TYPE: nucleic acid	
23	(C) STRANDEDNESS: double	
	. (D) TOPOLOGY: linear	
	Art. T	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :500:	,
	GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT	50
35	GCTCCCCACA TGGCGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA	100
	ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG	150

TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG

CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG

•	GTGGAGCTGT	260
	(2) INFORMATION FOR SEQ ID :501:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 268 base pairs	
•	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :501:	
15	AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT	50
	TAAATNCGTT GCTACAAAGT GTTTTGTTTC TCTAAAAAGT AGTTTTTGCA	100
20	TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTTGCT TTATATACAA	· 150
20	CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA	200
	CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA	250
25	ACCATGGCTT GCCCAAAT	268
	(2) INFORMATION FOR SEQ ID :502:	
	(i) SEQUENCE CHARACTERISTICS:	
30 -	(A) LENGTH: 152 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :502:	
	AAAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG	50
40	GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTGTAGAGAC	100

•	GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA	15
	cc	15
5	(2) INFORMATION FOR SEQ ID :503:	
	(i) SEQUENCE CHARACTERISTICS:	
'	(A) LENGTH: 141 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :503:	
	CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC	50
0.0	TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA	100
20	NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T	14:
	(2) INFORMATION FOR SEQ ID :504:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 107 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	^
30		
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :504:	
35	CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC	50
	GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG	100
	GCCGAGC	107
40	10	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
;		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :505:	
10	ACCCTCTTCT GATAAATTTG AGGGCCCGTT TGTCCTTGGA GACCTTCAGT	50
	AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT	100
15	GTCCCGCACG AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG	150
	CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTT GAG	193
20	(2) INFORMATION FOR SEQ ID :506:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 274 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	4	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :506:	
30	ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTTCCTACA	50
	TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT	100
.35	TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT	150
	GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT	200
40	TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA	250
40	TGACACAAAT CCAAACAAGA TGCA	274

265

	(2) INFORMATION FOR SEQ ID :507:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 281 base pairs	
5	(B) TYPE: nucleic acid	
-	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•	. e.,	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :507:	
	CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA	50
15	AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA	100
	GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA	150
20	AGTGGTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA	200
20	CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA	250
	CCATTGAGAA GATGCAGGAG TAAAGTATTA T	281
25	(2) INFORMATION FOR SEQ ID :508:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 180 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :508:	
	AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG	50
40	CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA	100
-T U		

GCAGAGGGGA CAGAGATGAT GACCCTTTCG CTCCCCCTG CAAATGAGCC

	.•	CCAGCCTTCT CCATGGTGGT GAAGACGCCA	180
		(2) INFORMATION FOR SEQ ID :509:	
5		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 104 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	•
		(D) TOPOLOGY: linear	
10			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :509:	
15	٠	AAATGCAAAA CTCACCGTGC ACACTCCTAG ATCCCTGCCA CAAAGAAATC	50
		TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT	. 100
		ATTT	104
20		(2) INFORMATION FOR SEQ ID :510:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 171 base pairs	
25		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
30		(xi) SEQUENCE DESCRIPTION: SEQ ID :510:	
		GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG	50
35		GGAAGCTAGA GCCAGAATCA GGAAAATCTG TTTCCTCGTC CCCAGACTCC	100
		CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA	150
		GACTTGCATC TGNATCTTGN A	171
40		(2) INFORMATION FOR SEQ ID :511:	_ , _

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 255 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
, 5	(D) TOPOLOGY: linear	
ì		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :511:	
10		
	ACTGTACCTA TCATCCTGAA AAACTTTATG GGGGAGAAAG GTCAGCAGCT	50
	TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGCGTATTCT ACTTTAACTA	100
15	AATGTAAGGA AGAAAATATA CAAGCCCATA TTTAATGTAT TTCTATNCGA	150
	GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT	200
	GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG	250
20	GATTA	255
	(2) INFORMATION FOR SEQ ID :512:	
ع در	(;) CROURNOR CUADACTERICE.	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
,	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :512:	
35	GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT	50
	TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT	. 100
	AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTTGATTT GTGTAACTTG	150
40	ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTTCATA AGCTGCTTTT	200

	GAGCTTTGTC	210
	(2) INFORMATION FOR SEQ ID :513:	
5	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 222 base pairs	
•	(B) TYPE: nucleic acid	
*	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
		•
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :513:	
15	CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA	50
	AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG	100
20	AACAGGGATT CTTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA	150
20	AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG	200
	AAGAAACAAA CGTGTGCATC CT	222
[‡] 25	(2) INFORMATION FOR SEQ ID :514:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 240 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :514:	
	GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT	50
	GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC	100
40		150

	CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC	200
	CTAGTCAGGA CCACAACTCT TAAACCTCAT AGCNAAATAT	240
. 5	(2) INFORMATION FOR SEQ ID :515:	
	(i) SEQUENCE CHARACTERISTICS:	
*	(A) LENGTH: 183 base pairs	
•	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :515:	
	CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA	50
20	ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA	100
	TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG	150
	TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG	183
25	(2) INFORMATION FOR SEQ ID :516:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 215 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
25	A TANKENOR PROGRESSION OF THE SAC	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :516:	
	TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA	50
40	CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATACACACG	100
- -	AACACTCATA CACACANGCT TGTGCACACA TGTTCATGCA CATGCATGCA	150

	CTCACACTCA TACAAACGCA CATTTAAACA CGTGTGNACA NTGTACTCAG	200
	ACACACAG GTGTG	215
, 5	(2) INFORMATION FOR SEQ ID :517:	
•	(i) SEQUENCE CHARACTERISTICS:	
,	(A) LENGTH: 181 base pairs	
•	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :517:	
	TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA	50
20	GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG	100
20	TGTCGCAGTG AGACAAACAC ACATACAGAC CACACAGA CCACCACCTC	150
	AATCATGGGC CCTAGCCGNC CTNGTAATAC G	181
¹ 25	(2) INFORMATION FOR SEQ ID :518:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 260 base pairs	
•	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :518:	
	ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT	50
	GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT	100
40	AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA	150

	. •	AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT	200
		CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA	250
, 5		CCTGGCAACT	260
		(2) INFORMATION FOR SEQ ID :519:	
		(i) SEQUENCE CHARACTERISTICS:	
10		(A) LENGTH: 115 base pairs	•
10		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
		(5) 10:020011 12::021	
15			
13			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :519:	
20		AAGCTAATAC AATGGTCATT TCCAGACAAA TTTAAAGGAA ACACTAAGGC	50
·20		TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA	100
	-	CATGCTCTTT TTTTA	115
¹ 25		(2) INFORMATION FOR SEQ ID :520:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 175 base pairs	
		(B) TYPE: nucleic acid	
30		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: linear	
35		(xi) SEQUENCE DESCRIPTION: SEQ ID :520:	
		CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTCGCAGA	50
40		AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA	100
		CONCNUNCT TOTOCONOTAC CARTOCONICA TOTOLOTORA COCTONATIVO	150

	GACTNATAGN TNGACCCACC TGTGA	175
	(2) INFORMATION FOR SEQ ID :521:	
5	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 136 base pairs	
	(B) TYPE: nucleic acid	
,	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :521:	
15	ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT	50
	TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG	100
	TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA	136
20		
	(2) INFORMATION FOR SEQ ID :522:	
	(i) CECUENCE CUADACTERICS	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 200 base pairs (B) TYPE: nucleic acid	
23	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) Torobodi. Timeat	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :522:	,
	AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG	50
35	GATATATTTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT	100
	GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC	150
	TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC	200
40	•	
	(2) INFORMATION FOR SEQ ID :523:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
, 5	(D) TOPOLOGY: linear	
;		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :523:	
10	AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT	50
	CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA	100
15	CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC	150
	ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA	200
	CATA	204
20	(2) INFORMATION FOR SEQ ID :524:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :524:	
v	ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT	50
35	GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC	100
	GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA	150
40	GAGGTCAATG TATCATCA	168
70	/2) INFORMATION FOR SEC. ID . F25.	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 291 base pairs	
	(B) TYPE: nucleic acid	,
	(C) STRANDEDNESS: double	
, 5	(D) TOPOLOGY: linear	
•		
;		
•	A CONTRACT PROPERTIES OF TRACES	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :525:	
10	AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT	5(
	AMOIGITOI TIAMMOOGO TOTOGTOGT MITTERCOMO CIMENOSTO	
	AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA	100
	•	
15	GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC	150
	•	
	ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT	200
		25.
20	TTATCTCCCT CTGCATTCAG ACCAGGCTCC TTAGTGCACT CATCAGACTA	250
20	TCGCTGCCCC TGCTGTCTGC TGTTGAGCCT TCACCACCAC T	29:
	1000100000 100101010 10110.10001 101.100.100	
	(2) INFORMATION FOR SEQ ID :526:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 207 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :526:	
	, , , , , , , , , , , , , , , , , , , ,	
35	CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACTCA	50
	TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC	100
	CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG	150
40	> 0.00m20.00m, 0.00m20.00, 0.00m20.00, mm.) 0.000.00m, 2.001.201.00m	20
	AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT	200

	GGGAAGC	207
	(2) INFORMATION FOR SEQ ID :527:	
5	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 218 base pairs	
,	(B) TYPE: nucleic acid	
ı	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :527:	
15	AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC	. 50
	AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC	100
20	CCAGCCAGAC TACATTTCCT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC	150
20	CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC	200
	CTCTGACCCA GCTTCACC	218
25	(2) INFORMATION FOR SEQ ID :528:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 229 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :528:	
	AACCTNATGA CTCTCCATCC CCTTGAACCA AACATCTAGC ACTCAGCTCC	50
	AGCATATTTC ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT	100
40	GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC	150

	CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT	200
	TTTACACCCA GTGTGTAAGC CAGAAGGGC	229
, 5	(2) INFORMATION FOR SEQ ID :529:	
· .	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 117 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :529:	
	ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA	50
20	ACAAGTGCAG GTTTTTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC	100
20	CTTAGCCTCT TTGCTTC	117
	(2) INFORMATION FOR SEQ ID :530:	
25	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 179 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :530:	
35	TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT	50
•	GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT	100
•	AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA	150
40	TATGCACATG CTGGTGCTAC CCTCTCACT	179

	(2) INFORMATION FOR SEQ ID :531:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 204 base pairs	
5	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
,		•
	en de la companya de La companya de la co	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :531:	
	AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAAT ATCTTCTCAG	50
15	CATTCAAAAC AAAACGCATA AGTCATTCCT AACTTNAGAG CTTTATAGCA	100
	TTTTCCTAGA CAGGAAGGGA AAAAACAGTT AGCATTTAAA AGTCCGGAAA	150
20	GCTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTTG TCCAAATCCC	200
	TTAT	204
	(2) INFORMATION FOR SEQ ID :532:	
¹ 25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 183 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :532:	
35	AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC	50
	CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC	100
40	CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAAATACC	150
	CTTTCTTCAA AACTTAGCTC TGAATGGAGA AAC	183

	(2) INFORMATION FOR SEQ ID :533:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 287 base pairs	
. 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	· ·	•
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :533:	
	GAAACAAGTT CTCGCTCATC CCTGCATTTC TGCCAACTTC AGCTTGCAAT	50
15	ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC	100
	TOTTTCACAA CACTTCTCTC TTTTCCCACACAA ACCCTTCCCTT	
	TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG	150
	TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG	200
20		
	GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT	250
	AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT	287
25	(2) INFORMATION FOR SEQ ID :534:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 154 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :534:	
	(
	AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT	50
	GACTTTTTGC AGTCAGTTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG	100
40		
	GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTCT	150

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	TTAG	154
	(2) INFORMATION FOR SEQ ID :535:	
, 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 212 base pairs	
:	(B) TYPE: nucleic acid	
·	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :535:	
15	GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG	50
	GGCCTATTTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA	100
, .		
20	TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG	150
	GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC	200
	CTAGGAAGGC AC	212
25	(2) INFORMATION FOR SEQ ID :536:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 168 base pairs	٠
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :536:	
	•	•
	GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT	50
	ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC	100
40		
	CTGCCCCTTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCCT	150

.•	NTCGGCAGTT GTCTTACT	168
	(2) INFORMATION FOR SEQ ID :537:	·
. 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 147 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :537:	
15	CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT	50
	GTTCCCTGCT GCCTGCCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA	100
20	GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNNTAA TGAAGTA	147
	(2) INFORMATION FOR SEQ ID :538:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 250 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :538:	٠
	GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG	50
35	GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT	100
•	GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT	150
40	GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA	200
- -	AATNAATGTA AACCCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC	250

(2) INFORMATION FOR SEQ ID :539:

	·	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 184 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
	*-	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :539:	
	(XI) SEQUENCE DESCRIPTION. SEQ ID .339.	
	AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT	50
	·	
15	GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTTCGGGG ATGGTGAATG	100
	·	
	CCCTTCTTTA ANNITAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC	150
	CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC	184
20	Cholodala doddidina handlaalli ddoc	101
	(2) INFORMATION FOR SEQ ID :540:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 154 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :540:	
	AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA	50
35	CCAGGGAAGT CACCCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT	100
	CATCATCATG TCTCCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC	150
	CATCATCAIG TOTOCOAGG NGIGOTIGON ANGAGATATI COGCCAAGCC	150
	AGAT	154
40		
	(2) INFORMATION FOR SEQ ID :541:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :541:	
10		
	AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA	50
	ATTTTGTTTT CTTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTTCCTTCA	100
	Allingilli Cilcididii Aliddiicha Adiacidaca Illicollan	. 200
15	TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA	150
	TGATTTGGTT ATACTGTGAA ACAGC	175
	(2) INFORMATION FOR SEQ ID :542:	
20		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 221 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :542:	
30		
	AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT	50
	CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC	100
•		
35	AGCCGTGCTG CTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT	150
	GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG	200
	AATCGCGACT GGCNAACAGA T	22
40		•
	(2) INFORMATION FOR SEQ ID :543:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	, seedool linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :543:	
10	2 - 3 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5	
	AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG	
	CAAAGTTAAG AAAGTTGAAG	50
	GAGAAACATA CCTTGAGAGG GGGTTTTCTT TAAAACTAGT GTTAGAAGCT	
		100
15	TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA	
		150
	TTTGACTTGT GCCGACATTG CAAACTTTNT GACAGG	•
		186
20	(2) INFORMATION FOR SEQ ID :544:	
20		·
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 153 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•	(vi) Charmes	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :544:	
	AGCATCCTTC CCA COMOGOGO	
	AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCTGCCT	50
	TGAACAGGCC ACAGCCCTAG CTCTT	
	TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA	100
35	CCGACAGGAG GAGGAGCCCT CCCMMONAGA	
	CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT	150
	GCC	
		153
	(2) INFORMATION FOR SEQ ID :545:	
40		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 161 base pairs	
	barra	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
3	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :545:	
	GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG	
10	GCCACCICCO CACCCGGGAG TCAAGGGTCG	. 50
	TGGTTCTGCC TTGAACACCC CACACCAC	
	TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT	100
	ACATCACCOCA ACCOLAGA	
	ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG	150
15		130
13	CCCAGGCCTG T	
		161
	(2) INFORMATION FOR SEQ ID :546:	
	(i) SEQUENCE CHARACTERISTICS:	•
20	(A) LENGTH: 188 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
	(a) iolobod: linear	
25		
	(vi) Spournes and	,
	(xi) SEQUENCE DESCRIPTION: SEQ ID :546:	•
	13m20com	
30	AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA	
30		50
	GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAACT TGGAAGGTCA	
•		100
	TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA	
	TORRATCCIT TGTGTACACA	150
35	TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA	
	CACTTTTA	188
	(2) INFORMATION FOR SEQ ID :547:	
	:547:	
	(i) SPOUDNOD OUT	•
40	(i) SEQUENCE CHARACTERISTICS:	
- -	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :547:	
	ATNOCTTOTO CATOCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTOTG	5
10	ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA	100
	GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT	150
	TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG	200
15	AATCACTCAT TTAGAAAA	218
	(2) INFORMATION FOR SEQ ID :548:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs	
	(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :548:	
30	GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT	46
.•	(2) INFORMATION FOR SEQ ID :549:	
	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 146 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	The state of the s	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

	•	
	AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG	50
	TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG	100
5	AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTTCNC	146
	(2) INFORMATION FOR SEQ ID :550:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 221 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :550:	
20	AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA	50
	ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT	100
	TGACTCTAGT CACCTTGTTG TGCGAGCAAG TACTAGGTCT TATTCATTCT	150
25	TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA	200
	TTTTAAAAAG ACAATGCTAG G	221
30	(2) INFORMATION FOR SEQ ID :551:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 116 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEC ID :551:	

40

ARACATCGTT TATTCATCCA GCAGTGTTGC TCAGCTCCTA CCTCTGTGCC

	AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG	100
•	GGGAGGGGT CATTGT	116
·5	(2) INFORMATION FOR SEQ ID :552:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 150 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(c) Tologodi. Illeat	
		·
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :552:	
	CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT	50
20	CAGTATCGCT CCTCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG	100
	TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT	150
	(2) INFORMATION FOR SEQ ID :553:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	·	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :553:	
35	ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT	50
	GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG	100
40	GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG	150
70	NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT	100

	(2) INFORMATION FOR SEQ ID :554:	·
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :554:	
	ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT	50
15	GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG	100
	GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG	150
20	NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC	198-
	(2) INFORMATION FOR SEQ ID :555:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 97 base pairs	•
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		•
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :555:	
	CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAAC TGAAGAACTT	50
35	GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG	97
•	(2) INFORMATION FOR SEQ ID :556:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 269 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :556:	
	TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT	50
10	GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA	100
10	GTCTTAGGAC ACAGAGACCA GGGTGTTGAA TTTTCTTCCC TGCCCCTAGG	150
•	CTGTTCAGGT CTTCCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT	200
15	CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT	250
٠	CTTCAAGGGT GATCTTGTT	269
20	(2) INFORMATION FOR SEQ ID :557:	
i	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
25	(D) IOPOLOGI: IIMeal	
		· •
	(xi) SEQUENCE DESCRIPTION: SEQ ID :557:	
30	(XI) SEQUENCE DESCRIPTION. SEQ ID 1337.	
30	ACTCCCTCAA GGTCGTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG	50
	ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT	100
35	GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC	150
	AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG	200
40	ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC	245
.,	(2) INFORMATION FOR SEQ ID :558:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	•
5	(D) TOPOLOGY: linear	
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :558:	
10		
	GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC	50
	ACAACCTTCG TTCCGCAGTT CATTAATCCG ACTCTGATGC TAAGGTGACA	100
	•	•
15	GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT	150
	GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT	183
	(2) INFORMATION FOR SEQ ID :559:	
20		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 116 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(') CROUDUCE PROGRESSION ORD TR .FFO.	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :559:	
30	GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG	50
	GIONICITIS GANASIGNOS INSCENSOS ANIANICOM GONGIINGGO	50
	AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA	100
		200
35	TGCTNAAGAA GCTGAC	116
	(2) INFORMATION FOR SEQ ID :560:	
	-	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 160 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :560:	
	CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC	50
	TGGATACGGC GACGGTTTCT CATTTGCCTT TGTCAGCTCT CATTCGCTGA	100
	GAGGCATAGA CCTTTTTGAT ATCATCAGGC TTTCCGTTTT TAGGAGCAAA	150
	ACAGCTTCTT	160
15	(2) INFORMATION FOR SEQ ID :561:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 101 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :561:	
	GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC	50
30	AAATGCACCC CGTTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAAACT	100
	G	101
	(2) INFORMATION FOR SEQ ID :562:	
35	(i) SEQUENCE CHARACTERISTICS:	
- -	(A) LENGTH: 183 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	· · · · · · · · · · · · · · · · · · ·	•

(xi) SEQUENCE DESCRIPTION: SEQ ID :562: ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTCGAT 50 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100 5 TATGAGGAGT GGAATTTTAG ATGTCTATTA CATTNGTCTT TTAAAAGAAA 150 183 AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 10 (2) INFORMATION FOR SEQ ID :563: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 187 base pairs (B) TYPE: nucleic acid 15 (C) STRANDEDNESS: double (D) TOPOLOGY: linear 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :563: AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA 100 25 AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150 GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187 30 (2) INFORMATION FOR SEQ ID :564: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid 35 (C) STRANDEDNESS: double (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

	GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA	50
,	CACAGAAAAA TGGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT	100
5	GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC	150
	AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC	200
•	AANGTGACTA TTC	213
10	(2) INFORMATION FOR SEQ ID :565:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 167 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :565:	
	TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG	50
25	GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG	100
	CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT	150
	TTCTTTTTT CCTTTAA	167
30		•
	(2) INFORMATION FOR SEQ ID :566:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 128 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

	GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT	50
•	GTATTACTTC CTNGTTACTA :GACCTCTAA TTCAATGGGG CCCTGCTGGT	100
· 5	TTGTCGATGA ATTGAGCAAC TGAGAACG	128
	(2) INFORMATION FOR SEQ ID :567:	
	(i) SEQUENCE CHARACTERISTICS:	•
10	(A) LENGTH: 202 base pairs	·
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) 10102011 1230	
1 5		
15 ,		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :567:	
	GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTTGGA	50
20	AAGTAGTCCT CAATCTTCGA TTTCCCAGCA AGGACTTTCT CAGCNAGCGA	100
	TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT	150
25	GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG	200
	NG	202
	(2) INFORMATION FOR SEQ ID :568:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 152 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
35	(D) TOPOLOGY: linear	
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :568:	

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA

	AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA	100
	CGGGTTACTT TCAAGGAAGA GTTGTTTTGT GACAAATTCT ACTCTTGATC	150
. 5	TA	152
	(2) INFORMATION FOR SEQ ID :569:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 181 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :569:	
	CAGGTCCGCG TGCTCTCCGC ACCACCCCAC TTCATTCCGG CCAAACCAAC	. 50
20	CGCACCCCTG AATTTCTCCG CAAATTTCCT GCCGGCAAGG TCCCAGCATT	100
	TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA	150
25	CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T	181
	(2) INFORMATION FOR SEQ ID :570:	
	(i) SEQUENCE CHARACTERISTICS:	•
30	(A) LENGTH: 157 base pairs	•
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
35		٠
	(xi) SEQUENCE DESCRIPTION: SEQ ID :570:	
· '	ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT	5
40	PAGE CONTEST GOOD OF THE CONTEST OF	10

	NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA	150
	ATGCTTT	157
5	(2) INFORMATION FOR SEQ ID :571:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 193 base pairs	
•	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :571:	
	GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA	50
•	AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC	100
20	AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC	150
	ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC	193
25	(2) INFORMATION FOR SEQ ID :572:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 179 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	:
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :572:	
	TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA	50
	GAAGGATTTG AGGAGGTTGG TGGAATTTGT TGAAGGAGAG GGCGAGGAAG	10
40	AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG	15

	CTTTCCTGTT TTAAACATGA AAGTGTGGC	179
	(2) INFORMATION FOR SEQ ID :573:	٠
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :573:	
15	AGGACCTCTA AGACATCCTT ATGACGACAG TTTTGTCCAA GGGGATATCC	50
	ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTTAAAAAGA	100
20	TTTTATTTCT GATCTTTTGG CGATCTTCTT CTTGCCCATG NNGCTGTTAC	150
	TTNGCNCGGG NAGCGGTTAA TTCTANCCGC TAGGTGTGC	189
	(2) INFORMATION FOR SEQ ID :574:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 262 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :574:	
35	GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG	50
	TARAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CARAGARTCG	100
	TCCTTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTTAA	150
40	ATGTATATCT TTTACGTCTC TACTCAGACC ATATTTNAAA GGGGCGCCTC	200

	ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTTG	250
	GTTCTAAGCA TT	262
5	(2) INFORMATION FOR SEQ ID :575:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :575:	
	CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT	50
	CCTGAC	56
20	(2) INFORMATION FOR SEQ ID :576:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 158 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :576:	
	GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT	50
35	CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC	100
	CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT	150
	CGTATCTT	. 158
40	(2) INFORMATION FOR SEQ ID :577:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 255 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
		,
		•
*		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :577:	
10 .		
	GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG	50
		100
	GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT	.100
		150
.15	CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG	
	AGTOTTOCTO CTGGACTTOT GGTCCTGGTA GGCTGTGCTT CATGCTCTCC	200
	AGTCTTCCTC CTGGACTTCT GGTCCTGGTA GGCTGTGCTT CATGGTCTG	
	TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA	250
20	IGICACCIGI ACIGIAAGON NOTHIIIIGEN GILLIO	•
20	CTTTG	255
	(2) INFORMATION FOR SEQ ID :578:	•
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 270 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
•		
	A CONTROL PROPERTY OF A CONTROL CONTRO	•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :578:	:
25	GAGGAGTCCA TGCCATCCTT GATGGAAAAG AAACTGAAGA GAAAAGACAG	50
35	GAGGAGICCA IGCCAICCII GAIGGAILLA ALLACIGATORIA	
	CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAG GAAAATATGA	100
	00101901110 11110101111111 111111111111	•
•	CATGATATCT TTGCTTTTGA GTTCCTCACG CTCTCTGAAT TTATTAGTTG	150
40		
	GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC	200

•	TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC	250
	TCTTGAGATA GTTTTGTTTT	270.
5	(2) INFORMATION FOR SEQ ID :579:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
•	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	·	•
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :579:	
-	GAGTTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA	50
	GGAGGTTGGG TGGATCTGTT GAAGGAGAG GNAGAAGAGG AGAGGAATGC	100
20	TARAGITARA ACGIARIARA GAIGCIGCIC ITACGGAAG	139
	(2) INFORMATION FOR SEQ ID :580:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :580:	
35	GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA	50
	TGTTCGATCC AATTTATTTC TTGGATAAGT TTTTCTTTCC TATNCCTNTN	100
46	GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA: A TATAGAGCTC	150
40	THE SOURCE MEMORIAGE OF	161

	(2) INFORMATION FOR SEQ ID :581:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 242 base pairs	
· 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :581:	
	CGGAGGCCC TGTTTGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA	50
15	TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT	100
	TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC	150
	CATTCTCCCT GGCTGCCAGC CCTTGAAGTC AGAACACCAT GGGAAAATTC	200
20		242
	AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA	242
	(2) INFORMATION FOR SEQ ID :582:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 37 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :582:	
35	GCATTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG	3'
	(2) INFORMATION FOR SEQ ID :583:	
	(i) SEQUENCE CHARACTERISTICS:	_
40	(A) LENGTH: 179 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :583:	
	GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG	50
	ACAAGAAACA CTTACCAACA AAAATATTTC AACAACCCCA AAATAACTTA	100
10	CTCACAAATA TGCAAAATTA TCTATGGCAT AGTATTTCGC ACTCGATGAC	150
	ATTTAGAGAT AAAAAATCAA ATGGAGCTT	179
15	(2) INFORMATION FOR SEQ ID :584:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :584:	
25		
	AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC	50
	AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA	100
30	GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT	150
	TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT	186
35	(2) INFORMATION FOR SEQ ID :585:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 180 base pairs	
•	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
7.0	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :585:	
	ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAACTA AACTACAAAC	50
5	GCACTCACAT CGCTATAATC CTTTTAAGGA CTTAAACTTT ACTCCATTAA	100
	GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCACTATA	150
10	CCTCGGAGAA CTTTCGCGTA ATAACCACGT	180
	(2) INFORMATION FOR SEQ ID :586:	
•	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 183 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :586:	
0.5	ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTTG GCTAANNNNN	50
25	NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC	100
	TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG	150
30	AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG	183
	(2) INFORMATION FOR SEQ ID :587:	*
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 280 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

••	AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN	50
	ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA	100.
5	GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT	150
•	GTGAACGTGC TAAGCGTACC CTCTCTCCA GCACCCAGGN CAGTATTNAG	200
	NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT	250
10	GAGACTGATG TGACNTTCCT GGGACTGNCA	280
	(2) INFORMATION FOR SEQ ID :588:	
15	(i) SEQUENCE CHARACTERISTICS:	
13	(A) LENGTH: 371 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	*
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :588:	
25	GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA	50
	CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC	100
	TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC	150
30	AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT	200
	TNTTTTGTTG CTTTTTGGGG TATTTTCATT AGTATTTCAG CAAATCTCAT	250
35	GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG	300
	ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT	350
40	GNGNNGCANG CTTANCTATG A	371
	(2) INFORMATION FOR SEQ ID :589:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :589:	
10	GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA	50
	TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT	100
15	GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA	150
	TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT	184
20	(2) INFORMATION FOR SEQ ID :590:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :590:	
30	GGGGGCCCGC CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCC	50
	NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTCATG GATANGGTGN	100
35	GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN	150
	AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG	200
	CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT	243
40	(2) INFORMATION FOR SEO ID :591:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :591:	•
10	ATTCGCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC	50
	NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN	100
15	NAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAAACTTT CAAATTCCGC	150
	CCCTTTNGGC NANGCCCAAC CANNCCCCCC CCCTTTTTNC CGNCCCANNC	200
	TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC	247
20	(2) INFORMATION FOR SEQ ID :592:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 425 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :592:	
	GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTTG	50
35	ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT	100
•	CCANGGATTA CGTTGCAATG TCTTCAAAAA TAGANAATTC ATTTTATATT	150
40	TCTNGATGAA ATATAATAGT ANCTNNGCTA CCTTTGGGAA TGTGACAAAA	200
40	TACTATGATG ATTACAACTC ATTAAAGCAT AAATNTGCAT GATTTAACTN	250

	CATGTTCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA	300
	TTTANGGCNT NNGTGCTTTG TAATGATTCG NCNTTAGGTG AAGGGNTACT	350
5 .	TTTNTNNTNC TTCNTAGTAG ATTNGNTTNN NTCTTTTTAA GAGGANTCNA	400
	NTTTCATGNG TAANCATCAT CTTTT	425
	(2) INFORMATION FOR SEQ ID :593:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 258 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :593:	
20	CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC	50
	GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA	100
25	CGCGTGTGAA CACATGCGCG CNNCGCGCNC GCGATNCAAA GCTGAAATGT	150
	GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAACAA CAATGAATGA	200
30	ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA	250
30	ANCAAAAG	258
	(2) INFORMATION FOR SEQ ID :594:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 215 base pairs	
	(B) TYPE: nucleic acid	
_	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

		DESCRIPTION:	SEQ	ID	:594:
(xi)	SEQUENCE	DESCRIPTION	_		

	(xi) SEQUENCE DESCRIPTION. DE	
•	GACCCTAACA ATATGTACAA AAATATAAAA TGTAAATAAA AAATACAAAC	50 _.
	AAATTTCCTT TTTAAAGTAC TTTTAAGAAA AAAAGCAGGG CCTTGGAAGT	100
5	TTTGGTTCTT TTTTCCTCCC CTGTTGCAAA TTCTCATGGT TTGGGTTGGG	150
	TGGTGGAGAG CGCGTGTCAT CTGCGGGTGC CTGCCCACGT GGGCGGGCGG	200
	TGGTGGAGAG	215
10	CTCTCTACTC GAAGG	
	(2) INFORMATION FOR SEQ ID :595:	
	(i) SEQUENCE CHARACTERISTICS:	•
15	(A) LENGTH: 272 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :595:	. •
25	GGGGCTGGTT TGGTCATCCG AGATCATTAA AAATGGCTGA CCCTAACAAT	50
	ATGTACAAAA ATATAAAATG TAAATAAAAA ATACAAACAA ATTTCCTTTT	100
	TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT	150
30	TTCCTCCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG	200
	CGTGTCATCT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT	250
35	CGARGGTGAC CACGTTTAGA TT	272
	(2) INFORMATION FOR SEQ ID :596:	
٠	(i) SEQUENCE CHARACTERISTICS:	
. 40	(A) LENGTH: 250 base pairs	
, 40	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :596:	
	GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTCA GCTTCCATTA	50
10	TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG	100
10	AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT	150
	CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC	200
15	CTTCCTCAAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG	250
	(2) INFORMATION FOR SEQ ID :597:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 225 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :597:	
30	CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA	50
	AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT	100
	ATCAAGAAAC CAGACTGTGA TGACTGGGAG AGCGGGCTGA ATGCAATGAG	150
35	TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGAACTGCAC	200
	AAACTGGCCA CTGACAAAAA TGACC	225
	(2) INFORMATION FOR SEQ ID :598:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	
	. (n) Denotin has been	

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :598:	
10	ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTTAGAT TTTCATTCAC	50
	AAAAAAGTC ATTCACATTT TACACTATAC ACGTTATGAT ATAATACAGG	100
	AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA	150
15	CGTGTTGTTC TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA	200
	CACCAGGGAC	210
20	(2) INFORMATION FOR SEQ ID :599:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(o) totologic linear	•
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :599:	
	AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC	50
٠	AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT	100
5	AGAAGTGAAA AAAAAA	116
	(2) INFORMATION FOR SEQ ID :600:	
•	(i) SEQUENCE CHARACTERISTICS:	
0	(A) LENGTH: 107 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :600:	
	ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC	50
	CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA	100
10	TGGCCTC	107
	(2) INFORMATION FOR SEQ ID :601:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 173 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :601:	
25	ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC	50
	GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT	100
20	TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC	150
30	ATTTTCTTTC CTTAGTGTAC CAA	173
	(2) INFORMATION FOR SEQ ID :602:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 216 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

• ••	(xi) SEQUENCE DESCRIPTION: SEQ ID :602:	
	GGAAGAGAAC ACATACACGA GGACCAGTAC CTGATGAGGA CAAGAGAGAT	50
5	GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT	100
	CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCCC TCCTCCCA	150
10	GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC	200
	AAGTACCCAG TAGGAG	216
	(2) INFORMATION FOR SEQ ID :603:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 213 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :603:	
25	GAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAAA TCACATATGT	50
	TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA	100
30	TTTCTAGGGC CCTTCTTGGG GAAAGGTTCA TATAATTTAG CATACATACA	150
	TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA	200
	TGGTAATATA ATG	213
35	(2) INFORMATION FOR SEQ ID :604:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 219 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	in a manage of the same	

(xi) SEQUENCE DESCRIPTION: SEQ ID :604: GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTCC 50 5 TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGACTGGACC TCTGGTCTCA 100 ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200 10 219 CTTCAAGAAG AAGAGCTGC (2) INFORMATION FOR SEQ ID :605: 15 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :605: 25 AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50 CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100 104 30 NNGA (2) INFORMATION FOR SEQ ID :606: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 189 base pairs 35 (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40

(xi) SEQUENCE DESCRIPTION: SEQ ID :606:

. •	AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTTACCAC	.50
	ANNTACAGAA TCTCCACCAT AGCATCAL.A CCAACTCTGA GGAACTTCGC	100
5	ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA	150
	TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA	189
	(2) INFORMATION FOR SEQ ID :607:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 171 base pairs	٠
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	•
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :607:	
20	GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA	50
	GAGCTCGTAT TTATCCTTTG CTTTNATNTG AGACCAAGCT AGCCCTGAGT	100
25	AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT	150
	GCCTTACGCA CATTCCTTTN T	171
20	(2) INFORMATION FOR SEQ ID :608:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 184 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
•	•	

(xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA

	TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAACTGTG	100
	ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA	150
· 5	TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA	184
	(2) INFORMATION FOR SEQ ID :609:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 191 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :609:	
	GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC	50
20	CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN	100
	TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC	150
25	TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T	191
•	(2) INFORMATION FOR SEQ ID :610:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :610:	
	GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT	56
40	GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT	10

	GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT	150
	AGGTATGATT TTATAGGNAT AA	172.
5	(2) INFORMATION FOR SEQ ID :611:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 51 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :611:	
	TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT	50
	T	51
20		
	(2) INFORMATION FOR SEQ ID :612:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 60 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		· .
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :612:	
	CGCCTGAAAC TTTGAGGATA AACTTTTTCA AAAAAATAAA ACAGTATCTC	50
35	TTAATCACTG	60
	(2) INFORMATION FOR SEQ ID :613:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 75 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :613:	
	TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT	50
	CCTGGGCGCA CAGCGAGACT GTCTC	75
10	(2) INFORMATION FOR SEQ ID :614:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 25 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :614:	
	ACGGGATTCT CTTCTTCGGC CGCCA	25
25	(2) INFORMATION FOR SEQ ID :615:	
•	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 72 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		٠
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :615:	
	GCAGTGTACT ATGTTCGCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA	50
	TAATATAGTG AGAACCCATC TC	72
40	(2) INFORMATION FOR SEQ ID :616:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	•.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :616:	
10		
	TCTAACTGAT TTCAAAGCAA ACTCTCTTT AATTAGGCTG CCTCTCCAGG	50
	GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA	100
	GOMMITTAG 1000A0010 COMOTOMOS TOTALONDO OTTOMOSOM	200
15	CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG	137
	(2) INFORMATION FOR SEQ ID :617:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		-
23		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :617:	
•	GCAGGGCAGT CTTGGTGTGC AGCCCCTCTC CTCTCTGTCC CCTGACACTC	5 C
30		
	CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT	100
	CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTCAC	139
35	/2) INFORMATION FOR CEO ID .610.	•
33	(2) INFORMATION FOR SEQ ID :618:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :618:	
	TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG	50
5	TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG	100
	CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNNCAC CTCTCNNCTG	150
10	ANNNNCCCAA CCAGCCCCAT TNCCAACA	178
	(2) INFORMATION FOR SEQ ID :619:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 73 base pairs	
,	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
20	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :619:	
25	ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC	50
23	TTCTGCGGCC GCCACCGCGT GGA	73
	(2) INFORMATION FOR SEQ ID :620:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :620:	
40	TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA	50
	AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT	100

	AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT	139
	(2) INFORMATION FOR SEQ ID :621:	
5	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 123 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :621:	
15	TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCT	50
	GGAAATGAGC TAAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNNCC	100
	CACTTCCTCC CATGCCCTCC AAA	123
20	(2) INFORMATION FOR SEQ ID :622:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 173 base pairs	
25	(B) TYPE: nucleic acid	
23	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :622:	
	CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA	50
35	AAAACATTTC NNGAGGAATT TTCAATTTCC AGCTTAAAGA ACNNNCCCAC	100
	CAACATAACC AATTTATGAA ANNNAATTCA TTAAAAGGTA TAGAACCTCT	150
40	TGTNNNCATG ATGGCAAGGG ACA	173
40	(2) INFORMATION FOR SEQ ID :623:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 112 bas pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :623:	
10		
	TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGGC	50
•	GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTTAC TAGAGCAACT	100
15	TGTCAGTAGA TT	112
	AND THEORY MADE FOR SEC. ID 46244	
	(2) INFORMATION FOR SEQ ID :624:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 119 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
23		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :624:	
•	ACTOCTTOTG COCCOGTTOT TOTAGTGAGA GGGGCGGACA AGGGGGCGGC	50
30	ACTULITUE COCCURTO TOTALISADA GOGGEGANA ACCUCACA	
	GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG	100
		• • •
	AGGTCTGCAT CCCCTCCCC	119
35	(2) INFORMATION FOR SEQ ID :625:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 39 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEO ID :625:	
' 5	AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC	39
5	(2) INFORMATION FOR SEQ ID :626:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	\cdot .	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :626:	
	CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA	50
20	ATAAAAATCT GAAAACATCC CC	72
	(2) INFORMATION FOR SEQ ID :627:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 153 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :627:	r
35	CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG	50
	AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT	100
٠.	CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC	150
10	AGT	153

(2) INFORMATION FOR SEQ ID :628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :628:	
10	(XI) SEQUENCE DESCRIPTION. SEQ ID :028:	
	AAAAGAAGTA GGTCGTGTCG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG	50
	GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA	100
15	CCGGCAGC	108
	(2) INFORMATION FOR SEQ ID :629:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 95 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :629:	
30	TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA	50
30	CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA	95
	(2) INFORMATION FOR SEQ ID :630:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	·	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :630:	
	CCAGCNCCGA AAAGCCAAGA CTTCATCAAC TACATAGGTC TTACCATTGA	50
5	CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT	100
	AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTG	139
	(2) INFORMATION FOR SEQ ID :631:	
10	/:\ CROHENCE CUADACTEDISTICS.	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :631:	
20	CCACCGCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC	50
	TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA	100
25	GCTGAAGTGG TGTGCTT	117
	(2) INFORMATION FOR SEQ ID :632:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 161 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :632:	
٠.		
40	CCAGCNCCGA AAAGCCAAGA CTTCATGAAC TACATAGGTC TTACCATTGA	50
70		

	AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTGA GGCCGCCATT	150
	GGAAGATGAA A	161
5	(2) INFORMATION FOR SEQ ID :633:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 97 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	\cdot	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :633:	
	COMO ONO COLO DE COLO	
	CCTGCNCCGA CGATGCCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA	50
	ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC	
20	TOTOLIMINON GRATARACTI CACCAGAAA AACAAAC	97
	(2) INFORMATION FOR SEQ ID :634:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
25	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	•	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :634:	
	CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC	
	THE CONTROL OF THE CO	50
35	TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC	100
		100
	TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA	150
	CANCAMAMOM AMOONAGES SEED	
40	GAAGATATGT ATGCAACGTT CATTCAAA	178
- •	(2) INFORMATION FOR SEO ID :635:	
	;,	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5 .	(D) TOPOLOGY: linear	•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :635:	
10		
	CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC	50
	CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA	90
15	(2) INFORMATION FOR SEQ ID :636:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 101 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :636:	•
	CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG	50
•	CAGGAGACAC AGACAATAGI CACIACATCA CACGGIIGII GIIIGGGAA	50
	GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC	100
30	T	101
		202
	(2) INFORMATION FOR SEQ ID :637:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 70 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :637:	• •
	CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT	50
5	TTTAATAAAG CACAGCACAA	70
	(2) INFORMATION FOR SEQ ID :638:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 160 base pairs	•
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :638:	
20	CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA	50
	ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG	100
	TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC	150
25	TCGGAGCTCG	160
	(2) INFORMATION FOR SEQ ID :639:	
	(i) SEQUENCE CHARACTERISTICS:	-
30	(A) LENGTH: 138 base pairs	
	(B) TYPE: nucleic acid	
·	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :639:	
40	CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC	50
	CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC	100

-	CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA	138
	(2) INFORMATION FOR SEQ ID :640:	
5 .	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 80 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
	(b) 10F0L061. 22	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :640:	
15	CCGACCACCC CTTCCTTTTC TTCGTCCATC CAGCACAGCA	50
	GATTCTCTTC TGCGGCCGCC ACCGCGTGGA	80
00	(2) INFORMATION FOR SEQ ID :641:	
20	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 100 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :641:	
30 .	AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA	50
	GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA	100
35	(2) INFORMATION FOR SEQ ID :642:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 77 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :642:	•
-	AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA	50
	GTTAATGTTC CATCCATGCT GCTTAAA	77
	(2) INFORMATION FOR SEQ ID :643:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 127 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :643:	
20	CCAGCGCCGA GAGCAGCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT	50
• •	ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG	100
	GGCTACAAGG ACTCGCCCTC CGTCTGG	127
25	(2) INFORMATION FOR SEQ ID :644:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 116 base pairs	
30	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
35		,
	(xi) SEQUENCE DESCRIPTION: SEQ ID :644:	,
••	GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT	50
40	GAGGAGGTTT CTCACCCCAC AGATAACCCA AGACACAAAT GTGCAATTAA	100
	AAGTTTATTT TAGACC	. 116

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·	
(i) SEQUENCE CHARACTERISTICS:	•
(A) LENGTH: 182 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
·	
(xi) SEQUENCE DESCRIPTION: SEQ ID :645:	
(XI) SEQUENCE DESCRIPTION. DEG 12 TOTAL	
CCACCACCG ATTCGTGACC AAGAAGGCTC TGTGCATTCG GGTTTTCCAG	!
•	
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC	1
	•
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATACAAG	1
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT	1
Acherolius. Contraction Contra	
(2) INFORMATION FOR SEQ ID :646:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 66 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
·	
·	

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CCAGCGCCGA	GGTTGTATAT	TTCTAGGTGC	AGGTATATGA	TTGCCATATA	50
***************	CAAAAC				66

(2) INFORMATION FOR SEQ ID :647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

331

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :647:	
	CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT	50
10	GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT	93
10	(2) INFORMATION FOR SEQ ID :648:	
٠	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 114 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :648:	
	CCCCTTTTTG TCCCCACTGA GATGTATGAA GGTTTTGGTC TCCCTGGGAG	50
25	TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA	100
	AAAGTGCACA CCTT	114
	(2) INFORMATION FOR SEQ ID :649:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 81 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID :649:	
40	(, degenee belong, 110M, bbg ID :047;	

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG

	GGATTCTCTT CTGCGGCCGC CACCGCGTGG A	. 8:
	(2) INFORMATION FOR SEQ ID :650:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 159 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :650:	
15	AGGAGENEEG ACAAAAGACA CATTGGACET GTCAGETECT CTGTTTCACE	50
	AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT	100
20	GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT	150
	AGACTAGAG	159
	(2) INFORMATION FOR SEQ ID :651:	·
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 78 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
30		·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :651:	
35	CCGACCACCC CTTCCTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT	50
	CTCTTCTGCG GCCGCCACCG CTGGAGCT	70
		78 ~
	(2) INFORMATION FOR SEQ ID :652:	
40		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	

PCT/GB93/01467

333

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :652:	
	CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTTA	50
10	· .	
	AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT	100
	CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
		150
15	TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198
	(2) INFORMATION FOR SEQ ID :653:	
	(1) 2 0	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 224 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :653:	
	CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
30		
	ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
	GCATCTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
35	TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTTG	200
	TTGCTATAAT AACACTTTTC TTTT	224
•	(2) INFORMATION FOR SEQ ID :654:	
.40	· · · · · · · · · · · · · · · · · · ·	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 226 base pairs	•

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
_		
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :654:	
10	CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT	50
	GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC	100
	CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA	150
15	AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTTGGTTT	200
	CTGAGCGCAT AAAGCTAAGG AGGGGT	226
20	(2) INFORMATION FOR SEQ ID :655:	,
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 167 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :655:	
30	TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTCA	5
	TTTGGTAACC TGTTTAGAAT TATAAAAATC ATTTCATTTG GCCCAGCCCA	10
35	TACGCCCAAG AGAAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT	15
•	CTTACAAAAT GCATATT	16
40	(2) INFORMATION FOR SEQ ID :656:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	

•	(B) TIPE. NACICES EST	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
·5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :656:	
•	·	50
	CCACCCTTC CTTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT	50
10		72
	TCTGCGGCCG CCACCGCGTG GA	, -
	(2) INFORMATION FOR SEQ ID :657:	
	A STATE OF THE PROPERTY OF A	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	·
	(D) TOPOLOGY: linear	
	(D) TOPOLOGI: IIIIear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :657:	
	(02) 222233	
25	AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA	50
	TACAGAACAA AAAAACTTTC CCTTTTTAAA ACTAATGTTA CAAATCTGTA	100
	·.	
•	TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAT AAGGTGTATA	150
30	•	
	GTACAATGTA TTCTAAAACT GTTCCGCC	178
	(2) INFORMATION FOR SEQ ID :658:	
35	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 76 base pairs	
	(B) TYPE: nucleic acid	
٠,	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :658:	٠
	CCGACCACCC CTTCCTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT	50
5	CTCTTCTGCG GCCGCCACCG CGTGGA	76
	(2) INFORMATION FOR SEQ ID :659:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 68 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :659:	
20	GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT	50
20	AACAAAAACC NTGAAAAC	68
	(2) INFORMATION FOR SEQ ID :660:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 151 base pairs	
	(B) TYPE: nucleic acid	÷
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :660:	
35	CCCAAACTTC TTTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT	50
	TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT	100
40	AAACACTGAT CAAACTCAGT TGTCCTTACG TTAGCATTAC TCTGTCATAG	150
	c	151

	(2) INFORMATION FOR SEQ ID :661:	•
	(-, -, -, -, -, -, -, -, -, -, -, -, -, -	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 245 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :661:	
	AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAACTTCAG CCACGTCTCC	50
15	TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT	100
	CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG	150
20	TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC	200
	TTCACTGTGC CTGCTGAGTC AGCTTGCATC TGCGCCTTCG GTGCG	245
<i>:</i>	(2) INFORMATION FOR SEQ ID :662:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
30 .		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :662:	
35	GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
	AATAAAAACM TGAAAACACC CC	72
-	(2) INFORMATION FOR SEQ ID :663:	
40	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 88 base pairs

	(B) Tipe: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		,
5		
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :663:	
	,	
	GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC	50
10		50
	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88
	(2) INFORMATION FOR SEQ ID :664:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
,	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :664:	
25	GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA	50
	GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC	100
	CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG	150
30		
	CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG	200
	CGGATAGTCA CACTCCCTGC CGA	223
•		•
15	(2) INFORMATION FOR SEQ ID :665:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 70 base pairs	
	(B) TYPE: nucleic acid	
0	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :665:	
	GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
5	AATAAAAATC TGAAAACACC	. 70
	(2) INFORMATION FOR SEQ ID :666:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 118 base pairs	•
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :666:	
20	GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA	50
20		
	TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCACC	100
	TTTCTACGTA CCGTATAG	118
25	(2) INFORMATION FOR SEQ ID :667:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 88 base pairs	
30	(B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	•	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :667:	
	GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC	50
40	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88
	(2) INFORMATION FOR SEQ ID :668:	

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 59 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :668:	
10		
	GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTTGATCTTC AACTCTGCAT	50
	ACAAGCAGA	59
	ACARGEAGA	29
15	(2) INFORMATION FOR SEQ ID :669:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :669:	
	(XI) DEGODACE DESCRIPTION. SEQ ID :009:	
	GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA	50
	•	
	CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG	100
30		
	CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC	150
	GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC	200
25	OMOGRACIONA ACCOMA COMO DO COM	
35	CTGCTCCCAG AGCCCACTTT TTT	223
	(2) INFORMATION FOR SEQ ID :670:	•
	(2) 111011111011101110110101	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 37 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

Ś	(xi) SEQUENCE DESCRIPTION: SEQ ID :670:	٠
	GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC	3
10	(2) INFORMATION FOR SEQ ID :671:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 37 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(2)	
		• .
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :671:	
	GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC	. 3
	(2) INFORMATION FOR SEQ ID :672:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 59 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :672:	
35	GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT	50
	ACAAGCAGA	59
:	(2) INFORMATION FOR SEQ ID :673:	
40		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :673:	•
	GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT	50
10	GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG	100
	GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC	150
15	CAAAGTATTA AAAGCAACTT TGCAATT	177
	(2) INFORMATION FOR SEQ ID :674:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 77 base pairs	
	(B) TYPE: nucleic acid	٠
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :674:	
30	GCCTGCGCCG AGCACAAGAC AATGACGAAC ATTTTAAAAA AAAAGAATGA	50
	CGCACATTTT AATAAAGCAC AGCACAA	77
35	(2) INFORMATION FOR SEQ ID :675:	
- -	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 176 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :675:	•
	GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG	50-
5	CCGTAACTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC	100
	ACCGCATCAC ATCGAGTGAT TATAGAAATC CATACACACA CCGATTGCAT	. 150
10	AAAATCTTTT TTTAGGAAAA AAACAC	176
10	(2) INFORMATION FOR SEQ ID :676:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 141 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		٠
20		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :676:	
	GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG	50
25	CCGTAACTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT	100
	ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C	141
20	(2) INFORMATION FOR SEQ ID :677:	
30	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 365 base pairs	·
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
35	(D) TOPOLOGY: linear	
•		
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :677:	
40		
	CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GGCGCTGACC	50

	NOONOOONNO GONANGOONI NOONOIICEN CHCHGICENG MCACIGEACG	10
	CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA	15
· 5	CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG	20
	GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCGTGGAC	25
10	CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT	30
20	CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA	350
	TCCAGGTGCT GTAGA	36
15	(2) INFORMATION FOR SEQ ID :678:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :678:	
	GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
30	CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC	100
	GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA	150
	GCCTTGCCCG CGAGTGCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG	200
35	TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCCGCGGAC	250
	CTGCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG	300
40	TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGCGTGCGGT	350
	CATCTAGGTG CTGTAG	366

5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 253 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :679:	
	GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
15	CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA	100
	GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC	150
	CCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT	200
20	TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC	250
	TTG	253
25	(2) INFORMATION FOR SEQ ID :680:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 294 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :680:	
	GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG	50
40	GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC	100

CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT

. •	CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA	200
	AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA	250
5	GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCCTACGG GCTC	294
	(2) INFORMATION FOR SEQ ID :681:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 268 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :681:	
20	CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGCGC	50
	GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG	100
	CTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC	150
25	TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC	200
	TGCCAACCAG AACTGACACG CGACCTCCTG GGCGCTGACG CCATTAAAAC	250
30	CAACGTTGGC GCCCGGCG	268
	(2) INFORMATION FOR SEQ ID :682:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 354 base pairs	
35	(B) TYPE: nucleic acid	
·	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

	GCCACCGCCG AGGAAAACCG TGCACTGTTA GCCATGATCA ACCCCACCGT	. 50
	GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG	100 -
5	AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA	150
	AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCTGCT TTCACAGAAT	200
	TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTCACACGC CATAATGGCA	250
10	CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC	300
	CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA	350
15	TACA	354
	(2) INFORMATION FOR SEQ ID :683:	·
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 148 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :683:	
	CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTG	50
30	TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC	100
	AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT	148
35	(2) INFORMATION FOR SEQ ID :684:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 307 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	

	·	•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :684:	
5	AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA	5
J	CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG	10
	CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG	15
10	GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA	20
•	TGCTCTTGCC ACACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC	25
15	TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT	30
	GTGAGGC	30
	(2) INFORMATION FOR SEQ ID :685:	
20	(i) SEQUENCE CHARACTERISTICS:	
-	(A) LENGTH: 174 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :685:	
30	CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG	50
	AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACTCTT AGCTGGCAAA	100
35	TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA	- 150
	GGAGCCATCT CTAGCGGGCC CTTC	174
,	(2) INFORMATION FOR SEQ ID :686:	
40 ·	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 106 base pairs	
	A Ph L. Million	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

	· · ·	
· 5		
J	(xi) SEQUENCE DESCRIPTION: SEQ ID :686:	
٠	ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA	50
10	CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT	100
	TATAAA	106
• •		
15	(2) INFORMATION FOR SEQ ID :687:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 97 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :687:	
	CAGATTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTTCCCCA	50
	GAGAAAAGGA AAGGGGGAAAA AACCCAACCC AAAACCA	97
30	(2) INFORMATION FOR SEQ ID :688:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
40		•

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

	GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC	. 50
	CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA	100
5	CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT	150
	GAATAGAGTC TAAGCGAACG AC	172
	(2) INFORMATION FOR SEQ ID :689:	·
10		
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 200 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
		•
00	(xi) SEQUENCE DESCRIPTION: SEQ ID :689:	
20		
	GCCACCGCCG AGCTCACCCC TGCGGTGCAC GCCTTCCTTG GACAAGTTTT	50
,	TCCCTTCTCC CACCCTTTTT CTCACCTCACACACACAC	
	TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC	100
25	TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC	
	TOUR TOUR CONCINENT TOUR CONTINUE TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR	150
	CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC	200
30	(2) INFORMATION FOR SEQ ID :690:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 81 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
9 3	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEO ID :690:	
	() ondormer procutition: DEO ID :PAD:	

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA

	ACACAAATTC ACAAGTGNTC TCAAAAAACT C	81
	(2) INFORMATION FOR SEQ ID :691:	
5	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 217 base pairs	
	(B) TYPE: nucleic acid	
-	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :691:	
15	TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA	50
	TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG	100
20	TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT	150
	GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC	200
	AGCTGACGCT CAAAAAG	217
25	(2) INFORMATION FOR SEQ ID :692:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :692:	
	CGGCCTTCTG GAAACCCATG AAAAAAAAA GTTCCGCACC TCCAAGGGGA	50
	GAAGAGTAAG AGACAGCTTT CA	. 72
40	(2) INFORMATION FOR SEQ ID :693:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs(B) TYPE: nucleic acid .(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :693:	
10	TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA	50
	GAAAAAGGCA AACAAGAAGA AGGAGGAACC CAAGCAGCTT TGCGGCTTCG	100
15	CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC	150
	GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTC	200
20	CCTTTGACCT AAGCCTACAG CAGGCCCCTT TTGTGCTTCC TTCCCCTCAG	250
20	GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCCTTC	300
	CCGATGCTTT TTGTTACCGT GGGGTTTGC	329
25	(2) INFORMATION FOR SEQ ID :694:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 296 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :694:	
	TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGG CCTGCGCCGA	50
	ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCC	100
40	GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGCGGACCA	150

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50

	GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA	200
	AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG	250
5	AGCCCACTTT TTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG	296
	(2) INFORMATION FOR SEQ ID :695:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :695:	
	GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG	50
20	AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG	100
	CGTGTCTTAG CACTAACCTC CTCCCTAGCC CCTTATTTGG TGGCAGAAGT	150
25	GGCCTCCACC CCTTCACCGT TTAAAAATAC TCCGTGGAGA AAAGAAAGCT	200
	TNAAGGAGTA G	211
	(2) INFORMATION FOR SEQ ID :696:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 92 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :696:	
40		

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC

	CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG	92
	(2) INFORMATION FOR SEQ ID :697:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 314 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :697:	
15	GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC	50
	CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG	100
	•	
	GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC	150
20		200
	ATAGTCAAGA GAAAGGATTT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA	200
	GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT	250
25	CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC	300
	GCATGCGTAC CTGT	314
	GERIGEGIAC CIGI	314
	(2) INFORMATION FOR SEQ ID :698:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 198 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(D) TOPOLOGI: Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :698:	
40		
	GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT	50

	GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT	100
	CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT	150
5	CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC	198
	(2) INFORMATION FOR SEQ ID :699:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 230 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :699:	
	GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG	50
20	CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAAGTGA ACAGAATGAC	100
	CTTCCTACGC ACAACACAAA CACCAGTTAA TGCTCCATCC ACGCTGCTTA	150
25	AAGAGCATTC CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCCACCC	200
	TTAGCCGGCA TGCTTACATT AATAGCTAGA	230
	(2) INFORMATION FOR SEQ ID :700:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :700:	
40	AGCAACAAAA ATGTTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT	50

	GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC	. 100
	AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCT	150
5	GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCTC ACTTGGCATG	200
	CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA	250
10	GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC	282
10	(2) INFORMATION FOR SEQ ID :701:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 255 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :701:	
	GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA	50
25	CATGGATCCG AATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG	100
	CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC	150
30	GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC	200
	CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC	250
	TTTCG	255
35	(2) INFORMATION FOR SEQ ID :702:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 89 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :702:	
_	GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA	50
5	CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC	89
	(2) INFORMATION FOR SEQ ID :703:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 96 base pairs	
	(B) TYPE: nucleic acid	·
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :703:	
20	GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA	50
	GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG	96
25	(2) INFORMATION FOR SEQ ID :704:	
25	(i) SEQUENCE CHARACTERISTICS:	,
	(A) LENGTH: 123 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :704:	
35	GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA	50
	ACACGGATCC GAATCACCTG GCCCGAAACC ACCTACCTAG CCATGATGAA	100
40	TGCTGAGGAC CCAGATGCAG TAC	123
	(2) INFORMATION FOR SEQ ID :705:	

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358

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

. 5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :705:	
10	GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG	50
	ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT	100
15	GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC	150
	ACATCACCGA GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG	200
	GACTAACCCT GTTCCCAGAG CCCACTTTTT TTCTTTTTCA GAAATAAAAC	250
20	AGCCTGTCTT TC	262
	(2) INFORMATION FOR SEQ ID :706:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 209 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :706:	
35	GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG	5(
33		
	AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG	100
40	CGTGTCTTAG CACTGCCCCC CTCCCTAGCC CCTTATTTGG CGGCGGAAGC	15
40	GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT	20

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	TCAGGGAGT	209
	(2) INFORMATION FOR SEQ ID :707:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 170 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :707:	
15	GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC	50
	TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAAGGAGGA	100
	ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTCACCTGT	150
20	GAGCCTGGAG CCAGTCCCAC	170
	(2) INFORMATION FOR SEQ ID :708:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 160 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :708:	
35	GCCACCGTCG AGGATTCAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG	50
	ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT	100
	TCTGCAGGCC GTTTCCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA	150
40	CCCAGAACCT	160

	(2) INFORMATION FOR SEQ ID : 709:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 51 base pars	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :709:	,
	GCCAGCACCG AGCAACCTGG GTCCAAATAA AAACTAAACT	50
15	G	51
	(2) INFORMATION FOR SEQ ID :710:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 64 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) TOPOLOGI: Timear	
25		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :710:	
22	GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA	50
30	CAGGATTCTC TTCT	64
	(2) INFORMATION FOR SEQ ID :711:	
35	(2 , 2 2 2 2 2	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 104 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :711:	
•	CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT	50
5	CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC	100
	TGGG	104
	(2) INFORMATION FOR SEQ ID :712:	
10		-
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 68 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :712:	
20	CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT	50
	TTGTTTTAG TTGAAGGC	68
25	(2) INFORMATION FOR SEQ ID :713:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 127 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :713:	
	AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT	50
40	GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT	100
	GTGCTTGGGT CGCTGTCTAC TGCTCCT	12

	(2) INFORMATION FOR SEQ ID :714:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 90 base pairs	
. 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :714:	
	CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC	50
15	CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT	90
	(2) INFORMATION FOR SEQ ID :715:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 69 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
23		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :715:	
	CCAGCGCCGA GGTTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA	50
30	•	
	ACAAAATCT GAAAACATC	. 69
	(2) INFORMATION FOR SEQ ID :716:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 102 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :716:	
-	GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA	50
5	CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT	100
	AA	102
	(2) INFORMATION FOR SEQ ID :717:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 124 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(5) 10102011 1211022	•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :717:	
20		
	AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT	. 50
•	GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT	100
	GCIGGCAIG AICTICAGCA IGIGCOGCCI CAIGCTIAAG CIGAAGIGGI	100
25	GTGCTTGGGA TACGCTGTCT ACAG	124
	(2) INFORMATION FOR SEQ ID :718:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 123 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :718:	
	GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA	50
40		
	TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG	100

	ACAAGGTCCC AAAGACAGCA GAA	123
	(2) INFORMATION FOR SEQ ID :719:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 54 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :719:	
15	ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC	50
	TTCT	54
	(2) INFORMATION FOR SEQ ID :720:	
20	·	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 117 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :720:	
30		
	GACCACAGGG CCTTCAATCC TTTTTTGTTT TCAACAGTCT TGCTGAATTA	50
	AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT	100
35	AATAAAACTG TGCACTC	117
	(2) INFORMATION FOR SEQ ID :721:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 55 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

365

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :721:	
	GACCACCCT TCCTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT	50.
10	CTTCT	55
10	(2) INFORMATION FOR SEQ ID :722:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 92 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :722:	
	GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC	50
25	ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT	92
	(2) INFORMATION FOR SEQ ID :723:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 55 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :723:	
	TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA	50
40	TCCCC	55

	(2) INFORMATION FOR SEQ ID : 724.	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :724:	
	GTGTACTATT AGCCATGGTC AACCCCACCG TGTTCTTCGA CATTGCCGTC	50
15	GACGGGCGAG CCCTTGGCGC GCGTCCTTTG AGCTGTTTGC AGACAAGGTC	100
	CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
20	TTTGGTTATA AGGG	164
20	(2) INFORMATION FOR SEQ ID :725:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 110 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		-
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :725:	
	GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC	50
35	ACACCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC	100
	AAGTTCAGTA	110
	(2) INFORMATION FOR SEQ ID :726	
40	(i) SEQUENCE CHARACTERISTICS:	
	(1) SEQUENCE CHARACTERISTICS:	

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367

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
_		
5	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :726:	
10	CCGTGTACTA TTAGCCATGG TCAACCCCAC CGTGTTCTTC GACATTGCCG	50
	TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG	100
	TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
15	TTTGGTTATA AGG	163
	(2) INFORMATION FOR SEQ ID :727:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 105 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :727:	
30	GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
	GTCACTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC	100
	CTGTT	105
35	(2) INFORMATION FOR SEQ ID :728:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :728:	
	GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG	50
5	ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT	100
	AGGAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTCGA GGCCGCCACT	150
10	GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA	186
	(2) INFORMATION FOR SEQ ID :729:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 167 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :729:	
	GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA	50
25	ATAAAAACCT GAAAACATCC CACCCGGGAA AAAAAAAAAA	100
	AAAAACACCC CCCCCCACA AAAAACTCAA ATTCCCCTCC CAAAAAACCC	150
30	CCTCAAAATC AAAAAAC	167
	(2) INFORMATION FOR SEQ ID :730:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 64 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		
40		

(xi) SEQUENCE DESCRIPTION: SEQ ID :730:

	GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA	50
	CAGGATTCTC TTCT	64
5	(2) INFORMATION FOR SEQ ID :731:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 96 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :731:	
	GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCGTGC ACCCCCGCTA	50
	GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG	96
20	(2) INFORMATION FOR SEQ ID :732:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 84 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID :732:	
	GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA	50
35	CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA	84
	(2) INFORMATION FOR SEQ ID :733:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 96 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(- /	

(D) TOPOLOGY: linear

. 5	(xi) SEQUENCE DESCRIPTION: SEQ ID :733:	
	GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA	. 50
10	GCGCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG	96
10	(2) INFORMATION FOR SEQ ID :734:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 96 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :734:	
	GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA	50
25	GCGCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG	96
	(2) INFORMATION FOR SEQ ID :735:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 97 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :735:	
	GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCCACT	50
40	ACCOUNTS OF THE TRANSPORT OF THE PROPERTY TRANSPORTED TO THE TRANSPORT OF THE PROPERTY TRANSPORTED TO THE PROPERTY	97

	(2) INFORMATION FOR SEQ ID :736:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 127 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :736:	
	GCCAGCGCCG ACCACAGGC CTTGAATCCT TTTTTGTTTT CAACAGTCTT	50
15	GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA	100
	TACAGCATTA ACAAAACCGC GCATCTC	127
20	(2) INFORMATION FOR SEQ ID :737:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 64 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	•
	·	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :737:	
30	GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA	50
	CAGGATTCTC TTCT	64
35	(2) INFORMATION FOR SEQ ID :738:	
	(i) SEQUENCE CHARACTERISTICS:	
-	(A) LENGTH: 88 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :738:	
	GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC	50
5	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88
	(2) INFORMATION FOR SEQ ID :739:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 95 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :739:	
20	GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCGGTGCA CCCCCGCTAG	50
	CGCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG	95
	(2) INFORMATION FOR SEQ ID :740:	
25		
	(i) SEQUENCE CHARACTERISTICS:	,
	(A) LENGTH: 245 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :740:	
35	\cdot	
	GCCACCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA	50
	GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA	100
40	CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCGAAGGA	150
	CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT	200

	CCGCCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA	245
	(2) INFORMATION FOR SEQ ID :741:	•
· 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 88 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :741:	
15	GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTCGTCTAT CACTCTCCCC	50
	AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG	88
20	(2) INFORMATION FOR SEQ ID :742:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 242 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	•	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :742:	
	GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC	50
	GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA	100
35	CTCTGATAGT CTTCATTCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG	150
	AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT	200
40	CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA	242
	(2) INFORMATION FOR SEQ ID :743:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 64 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	742.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :743:	
10	GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA	50
	CGGGATTCTC TTCT	64
	•	
15	(2) INFORMATION FOR SEQ ID :744:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 69 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		æ
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :744:	
23	(112)	
	GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT	50
		ــــــــــــــــــــــــــــــــــــــ
	AATAAAATT TGAAAACAT	69
30	(2) INFORMATION FOR SEQ ID :745:	
	(2) INFORMATION FOR BBy 15 (175)	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 74 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(I:) TOPOLOGY: linear	•
40	•	
. •	(xi) SEQUENCE DESCRIPTION: SEQ ID :745:	

	GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT	50
	AATAAAAATC TGAAAACATC CCAC	74
5	(2) INFORMATION FOR SEQ ID :746:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 88 base pairs	•
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :746:	
	GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCC	50
	AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG	88
20	(2) INFORMATION FOR SEQ ID :747:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 88 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	······································	
30 .	(xi) SEQUENCE DESCRIPTION: SEQ ID :747:	
	(XI) SEQUENCE DESCRIPTION. SEQ IS	
	GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC	50
35	AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG	88
-	(2) INFORMATION FOR SEQ ID :748:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :748:	
	GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT	50
	GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG	100
10	GCGAGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC	150
	CAAAGCATTA AAAGCAGCTT TGCAATTC	178
15	(2) INFORMATION FOR SEQ ID :749:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 235 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :749:	
	GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG	50
2.0	ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT	100
30	AGAAAGGCAT CTTTCGCCAG TGGATTCGCC CCAAGGTTGA GGCCGCCATT	150
	GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT	200
35	TGGCGCTGCT GCCTATAACA AACACTTTTT TTTTT	235
	(2) INFORMATION FOR SEQ ID :750:	
	(i) SEQUENCE CHARACTERISTICS:	٠,
40	(A) LENGTH: 87 base pairs	
	(B) TYPE: nucleic acid	
	. (C) STRANDEDNESS: double	

377

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :750:	
	GCCTACGCCG AAAACCCCTT CCTTTTTTC ATCCAGAAAA GCAAGAGAAA	50
	AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT	87
10	(2) INFORMATION FOR SEQ ID :751:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 170 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :751:	
	GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG	50
25	GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC	100
	AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC	150
	ATGCCAAAGA CACTCAAAGA	170
30	(2) INFORMATION FOR SEQ ID :752:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		
40		

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

	GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT	50
	AATAAAAAA TGAAAACACC CC	72
5	(2) INFORMATION FOR SEQ ID :753:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 122 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :753:	
	GCCAGCGCCG AGGACACCAA GAAGGTTTTG GACAGCGTGG GCATCGAGGC	50
20	GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAAACA	100
20	TTGAAGACGT TATTGNCCAG GA	122
	(2) INFORMATION FOR SEQ ID :754:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH 243 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :754:	
35	GCCACCGCCG ACTGAAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA	50
	GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC	100
40	AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG	150
*0	GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG	200

	CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT	243
•	(2) INFORMATION FOR SEQ ID :755:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 71 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :755:	٠
15	GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT	50
	AACAAAAACC TGAAAGCATC A	71
	(2) INFORMATION FOR SEQ ID :756:	
20	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :756:	
30	GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG	50
	GGCGCGCGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT	100
35	TAGTGCTTTT TCAGTGGGGC GGGGCGGGAA GCAGGCGGGA CCAGGCAGCC	150
	AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA	200
••	GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA	243
40	(2) INFORMATION FOR SEQ ID :757:	

	(I) SEQUENCE CHARACIERISTICS.	
	(A) LENGTH: 64 base pairs	
	(B) TYPE: nucleic acid	-
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :757:	
10		
	GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA	50
	CAGGATTCTC TTCC	64
15	(2) INFORMATION FOR SEQ ID :758:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	·	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :758:	
	GCCÁGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG	50
•	GGCGCGCGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT	100
30		
	TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC	150
	AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA	200
		243
35	GACGTCGACA ACCAGAACTG ACGTGCGACC TCCCGGGCGC CGA	243
	(2) INFORMATION FOR SEQ ID :759:	
	A CONTRACT OF THE CONTRACT OF	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 245 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :759:	
	GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG	50
	AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT	100
10	CTTCGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG	150
•	TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA	200
15	TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTC GGCCA	245
	(2) INFORMATION FOR SEQ ID :760:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 68 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
25		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :760:	
30	GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT	50
	AACAAAAACC NTGAAAAC	68
	(2) INFORMATION FOR SEQ ID :761:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 71 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :761:	
	GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
5	AATAAAAACT GAAAACACCC C	71
	(2) INFORMATION FOR SEQ ID :762:	
٠	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 88 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :762:	
22	GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC	50
20	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88
	(2) INFORMATION FOR SEQ ID :763:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
		,
	(xi) SEQUENCE DESCRIPTION: SEQ ID :763:	
35	GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA	50
	GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC	100
40	CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG	150
40	CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG	20

	CGGATAGTCA CACTCCCTGC CGA	223
	(2) INFORMATION FOR SEQ ID :764:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 70 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :764:	
15	GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
	•	
	AATAAAATC TGAAAACACC	70
	(2) INFORMATION FOR SEQ ID :765:	
20		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 118 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	() CECUENCE DESCRIPTION, SEC ID . 755.	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :765:	
30	GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA	50
	TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAA CCAAACCACC	100
35	TTTCTACGTA CCGTATAG	118
33	THE TROUBLE COURTED	110
	(2) INFORMATION FOR SEQ ID :766:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 88 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

384

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :766:	
	GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCC	50
	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88
10	(2) INFORMATION FOR SEQ ID :767:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 91 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :767:	
	GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTTGATCTTC AACTCTGCAT	50
25	ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T	91
	(2) INFORMATION FOR SEQ ID :768:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :768:	
	GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA	50
40		
	CAMPAGE CAMPAGE COMON MUCANA COM COCCANACO AMOCUCANO	100

	CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC	150
	GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC	200
5	CTGCTCCCAG AGCCCACTTT TTT	223
	(2) INFORMATION FOR SEQ ID :769:	
	(i) SEQUENCE CHARACTERISTICS:	-
10	(A) LENGTH: 37 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :769:	
	GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC	37
20		
	(2) INFORMATION FOR SEQ ID :770:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 37 base pairs	
25 .	(B) TYPE: nucleic acid	
23	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :770:	
	GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC	37
35	(2) INFORMATION FOR SEQ ID :771:	
• •	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 91 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(X1) SEQUENCE DESCRIPTION: SEQ ID ://I:	•
;	GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT	50
. 5	ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T	91
	(2) INFORMATION FOR SEQ ID :772:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :772:	
20	GCCTGCGCCG ANGCATTCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT	50
	GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG	100
	GTGAGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC	150
25	GIGROGGGI INGGGIIGG GAGIGITII INIII GAGIGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	
	CAAAGTATTA AAAGCAACTT TGCAATT	177
	(2) INFORMATION FOR SEQ ID :773:	
30	() GROUPINGE GUADACTERISETICS.	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 151 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
2 ×		
	() CROURNOR DECORIDATION, CPO ID -772.	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :773:	
40	***************************************	-

	GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC	100
	TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG	150
5	T	151
	(2) INFORMATION FOR SEQ ID :774:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 299 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
-	(xi) SEQUENCE DESCRIPTION: SEQ ID :774:	
20	ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTTCAAA CAGTGAACCA	50
	CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA	100
	CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC	150
25	ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG	200
	GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG	250
30	AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA	299
	(2) INFORMATION FOR SEQ ID :775:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 185 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
	·	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :775:

	TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG	50
	TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA	100
5	AACCGTATAT TTAAAATGAA TTACTAGAGA GGGAATGTAA TCATGGCAAA	150
	AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC	185
	(2) INFORMATION FOR SEQ ID :776:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 255 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
ė		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :776:	•
20	ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA	50
	TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC	100
25	ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA	150
,	AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT	200
	CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC	250
30	AACAT	255
•	(2) INFORMATION FOR SEQ ID :777:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 239 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	•	

WO 94/01548 PCT/GB93/01467

	(xi) SEQUENCE DESCRIPTION: SEQ ID :777:	
	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAAAATTTCG TTCTTGGCTG AATCGTGTTA	100
,	AACCGTTGTA CACAACGTAG TAAAATTCAT AACCCATCTG CATACCAATC	· 150
10	GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239
	(2) INFORMATION FOR SEQ ID :778:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 252 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :778:	
25	ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCGA ACATGCTACA	100
30	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG	150
	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTTAAGG ATGACTCAAC TTCGCCAACT CGGTTCCTCA TTAGGACAAC	250
35	TA	252
	(2) INFORMATION FOR SEQ ID :779:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 265 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

390

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :779:	
	TCGGATTTAT ACGGCTGTTA GTGCTATCGG CGTCTGGTAT GTGTTATATA	50
	TCGCCTATCG TTTTTTGGCC AATGGGCGTT GGCTACGCGG GGCAATGATT	100
10	GCCATCGTTT TTGTTATCTT GACTTATTTC GTCATTTTAA ATATTATTTA	150
	ACTATTTTAC AAATAAAGTG GTCAAATGGG ATATTTTGCC AAAAATAGAG	200
15	AAAGTGTTAG GCGGCCCACA GCTGGAGGAA GAGAAAGCGG CTGTGCATGA	250
	AGTTATTGCA CCCGC	265
	(2) INFORMATION FOR SEQ ID :780:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :780:	
	CTCAGCTGGA CCAAATTAGT TGAATTACTC ACCATCAATA AACTATAAAT	50
	GGCGCCAATG ACCAACCCGC CAACGATTCC CGTTGTCAAA GAACCTAATA	100
35	ACAAGTAACC AACCGCAGCC CCAACAAGCC CAACTAGGTT TAAAAAAACC	150
	AAGCAAAAGG CCAACTGTCC GTCGTTTATT GGATTGTATC TGCTCATATA	200
40	ACATTAAAAC TTAACCGTTG GCACTTCTTT CTCAGACCCG CCGATACTG	249
40	(2) INFORMATION FOR SEQ ID :781:	

(A) LENGTH: 188 base pairs .

(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

•	(C) STRANDEDNESS: double	
. 5	(D) TOPOLOGY: linear	
**	· :	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :781:	
10	GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG	50
	CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC	100
15	TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC	150
	TTCGACCTGA GCCACGCTC TGCCCAGGTT AAGGGCCA	188
	(2) INFORMATION FOR SEQ ID :782:	
20	4: A GROUPINGE OUR PROMEDICATION	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :782:	
	AATATTTATT TCATTTGTTT ACTACCACTT CATTTTATTT GTTTGCTGCT	50
	GCCGTTTTAT TTATTTTTAC TGAAAGTGAG AGGGAACTTT TGTGGCCTCC	100
35	AACCTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTTGG AACATCTAAC	150
	AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT	182
	(2) INFORMATION FOR SEQ ID :783:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 295 base pairs	
	/··/	

392

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		•
5		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :783:	
	(XI) DDQODNOD DDDONII IION, DIE ID 1/001	
	CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC	50
	CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC	50
10		
	CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT	100
	CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT	150
15	TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA	200
	CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG	250
	AGAGAATTCA AATGCGTGTT GGTGTTCCTG TTAGTACAAG CAGCA	295
20		
	(2) INFORMATION FOR SEQ ID :784:	
	(1) 111101111111111111111111111111111111	
	(i) SEQUENCE CHARACTERISTICS:	
0.5	(A) LENGTH: 295 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	•	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :784:	
	CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC	50
35	GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCACT TCAGAACCAG	100
	TACCTGATGT TGTTGGAATG GCAACCATTT GTGTCAAACG CACTGGTAGA	150
	INCUIGNIGI IGIIGGANIG GCANCCAIII GIGICAANCG CACIGGIAGA	130
	\	
	ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTTC TATTTCCATG	200
40		
	AACAATTCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT	250

	TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC	295
	(2) INFORMATION FOR SEQ ID :785:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 303 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
10		
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID :785:	
15	GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA	. 50
	CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTTC	100
20	ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC	150
	CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA	200
	GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT	250
25	GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA	300
	GTA	303
30	(2) INFORMATION FOR SEQ ID :786:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 255 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) Torobodi. Timedi	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :786:	
	TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT	50

	CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT	100
	ACATGAAGAA TGATGGTGTT CGTGGGGCCA TTAAGTACTA AGCCAAGAAG	150
5	TTATCACGAC AACCTATAAC TTGGGCCGAA TTAACTTGAT GATGCACGGG	200
	GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA	250
	CTGGC	255
10	(2) INFORMATION FOR SEQ ID :787:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 206 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :787:	
	(XI) SEQUENCE DESCRIPTION. SEQ ISO	
	CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG	50
25	TCAGAATCAA CAAAACTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG	100
	GGCATGATAC AAACCAGTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG	150
	ACTTATTTT ATTTTTTTT TTTTGGACAG ACTCCCTTTG TCCCCAGGCC	200
30		
	GGAGTG	206
	(2) INFORMATION FOR SEQ ID :788:	
25	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 260 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

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•	(xi) SEQUENCE DESCRIPTION: SEQ ID :788:	•
	ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT	50
5	CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG	100
	TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCGTGGA	150
	AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG	200
10	GAACAATTCC GCGACACCCT TCGTCTGACA AAAAACCTTC GTGACGCGTC	250
•	GAGTATCCGC	260
15	(2) INFORMATION FOR SEQ ID :789:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :789:	
•	AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC	50
20	TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT	100
30	GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT	150
	TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG	200
35	ATCGACGC	208
	(2) INFORMATION FOR SEQ ID :790:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 289 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :790:	
	AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT	50
	GAAAATACAT TGTTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC	100
10	ACTCTTGCTA TCGACCATCG TCGCGCTTTG GATGAACCGT CGTAAGTCAC	150
	AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT	200
15	TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG	250
	TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC	289
20	(2) INFORMATION FOR SEQ ID :791:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 232 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :791:	
30	TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAAATT TGGCAATTAA	50
	TTGCTCATTA TTAATGGTAG AGTTTCCATT AATGAAGTTG GAAAATACGG	100
35	TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT	150
•	GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA	200
40	CCARATTGAA GCACCTTATC TATGATCCGG GC	232
40	(2) INFORMATION FOR SEQ ID :792:	

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(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

•	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :792:	
10		
	TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC	50
	TGGTAATATC GAACAAACTA TTTTTAAGAA CTTGATTTCT GGCAACATTA	10
	1001AATATO OMIGIMIONI TITTIMOMI OTTOMIZZO COGNISSIONI	
15	AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG	150
	GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA	200
	TGCCTATTTC GCGAAGTATG GATCTAAATA AC	23:
20	IGGIAITIC GGGAAGTATG GATGTAAATA AG	25.
	(2) INFORMATION FOR SEQ ID :793:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 292 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30.		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :793:	•
-	GGGAACATAT CTTCACGGTA GTGANCCCAG TGACCAGATG TCTTATACAA	5
35	GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA	10
-		
	ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC	15
40	ATTTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA	20
40	ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTCACGTTC TTTAGCTTCT	25
	UPUNGICOUT GIOUCOUCOU UICAICCAGI AGIOUCAIIC IIIUACIICI	. ب

·	TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT	292
	(2) INFORMATION FOR SEQ ID :794:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 288 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :794:	
15	CAGCAGGCAC AACACCATCG GTTGTCGCTG AAAGTATTTT TAAGTCTTTG	50
	GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACTTATG CGGGTATGCA	100
20	TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG	150
	ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA	200
	GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC	250
25	CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC	288
	(2) INFORMATION FOR SEQ ID :795:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 258 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :795:	
40	GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT	.50
40	CGATAGACCC AAAAAGTGTT TTAACTGGAA AACACCTTAT GAGGTTTATT	100

•	TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT	150
	CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC	200
5	GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTTG CCCCGAGTGA	250
	TCGTCGGC	. 258
10	(2) INFORMATION FOR SEQ ID :796:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 270 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :796:	
20		50
	TGCTTCAAAG CCTGGCTTAA CCCGCTTGCC CACCAACTTC AATTATACCT	50
	GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC	100
25	CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC	150
	NAMES OF THE PROPERTY OF THE P	200
	ANTÁGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG	200
	AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG	250
30		
	CTCATGTAAC GCGACAATAT	270
	(2) INFORMATION FOR SEQ ID :797:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :797:	
	AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC	50
5	TTGTGTAGGT TGTCTGAAAC GGTCGCAGTC ACCGGTTAGC TTGATAAGTC	100
	AGGTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC	150
	AATCGCACTT TACATCATTA AGACCCTTAC TAGAAGTAAC TGGCCATCCT	200
10	GCCACCGCTT	210
	(2) INFORMATION FOR SEQ ID :798:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :798:	
25	ATCATAAGCG CTGGAACTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT	50
	GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA	100
20	CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA	150
30	TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCAAA TAACGAGACA	200
	AGTAGTTGAG CTAAATGC	218
35	(2) INFORMATION FOR SEQ ID :799:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 176 bass pa rs	
	(B) TYPE: nucleic e .d	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :799:	
5	CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG	50
	AGAATAGCAT TACCAAATGG AACAACGTGC TACAGTCAGG ATTAAAAAGA	100
	ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG	150
10	AACAATACAA CACTGAATTA CTCGGC	176
	(2) INFORMATION FOR SEQ ID :800:	
-	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 254 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :800:	
25	GCAATTGCTT AATTTGTTCT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA	50
23	CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA	100
	TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT	150
30	TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA	200
	GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT	250
35	TCGA ·	254
	(2) INFORMATION FOR SEQ ID :801:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 203 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :801:	
. 5	ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA	50
	TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT	100
	AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT	150
10	AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA	200
	ATG	203
15	(2) INFORMATION FOR SEQ ID :802:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 193 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :802:	
	GACACAACTG TGTTCACTAG CAACCTCAAA CAGACACCAT GGTGCACCTG	50
		•
	ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG	100
30	•	
•	GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG	150
	GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC	193
35	(2) INFORMATION FOR SEQ ID :803:	
33	(2) Intermitted tex and in terminal	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 290 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	

40

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :803:	
-	AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA	50
5	AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC	100
	AATAGCGTAC AGATTTTTCC GCATTAATCC GTGTTTATAT TAACAGATTC	150
10	GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA	200
	ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTTCTAAA	250
	CGATAACAAG AACCCCAGTA GGTAGTATAG CAGTCTTTAA	290
15	(2) INFORMATION FOR SEQ ID :804:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 256 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :804:	
	AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA	50
30	AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC	100
	AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT	150
26	CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCCTAC CACTTCCGGG	200
35	CCCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA	250
	ACAGGG	256

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID :805:

404

(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	() CROURNER DESCRIPTION, SEO ID . CO.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :805:	
10	AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAGTCT	50
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGCGGCG	100
15	AGGCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC AGAGATTCTT	150
	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG GGCAACCCTA	200
	AGACGAAGGC TCATGGCAAG AAAGTGTTCG GTGCCTTTAG TGATGACCTG	250
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286
	(2) INFORMATION FOR SEQ ID :806:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 291 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :806:	
35	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT ACACTGGCCT	50
30	CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA AAAAACTTCC	100
	ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT GTACAACAAA	150
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAG ACTCAGAGAT GTAATAGATG	200
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC AATATGAAAG	250

	TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C	291
	(2) INFORMATION FOR SEQ ID :807:	
. 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 276 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :807:	
15	AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTTATTAG GCAGAATCCA	50
	GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG	100
20	GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAAGAAAG CGAACTTAGC	150
	GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG	200
	GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC	250
25	ACAGACCAGC ACGTCGCCCA GGAGCC	276
	(2) INFORMATION FOR SEQ ID :808:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :808:	
40	GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT	50
	CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA	100

	ACATCGCTAG CTAATTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG	150
	AAGCTTGTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG	200
5	ACGTGATCGC TTATCGTA	218
	(2) INFORMATION FOR SEQ ID :809:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 276 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :809:	
20	AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA	50
	CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT	100
	TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCCC	150
25	TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC	200
	TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG	250
30	ACTAATGGCA AGCAAGTGCT AGACGC	276
	(2) INFORMATION FOR SEQ ID :810:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	-
	(D) TOPOLOGY: linear	
•		

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(xi) SEQUENCE DESCRIPTION: SEQ ID :810:

•	GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC	50
	CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCCTTCT	100
. 5	GAGGAGGCTT ACTGCTTTTC TTACTCGATT TATTTTTCAG AGTTTTCTTC	.150
	TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTTATTCT CCTCCATTT	199
	(2) INFORMATION FOR SEQ ID :811:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 254 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :811:	
20	(MI) EDGELMED DECOMINE DEG ID TOLL	
	AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA	50
	AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC	100
25		150
25	TGGGGGGCTT GGCGTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA	150
	GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT	200
	TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT	250
30		
	AAGT	254
	(2) INFORMATION FOR SEQ ID :812:	
	(2) 300 300 300 300 200 200 200 200 200 200	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 284 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
40		

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :812:	٠
	TTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA	50
5	CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA	100
	CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA	150
10	CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCACTTC CAAACAGGCA	200
10	ACCTGCACCG GAGGGGAGAC TTTTTCGCCA AAGCGACGGG CCAGCACACA	250
	GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA	284
15	(2) INFORMATION FOR SEQ ID :813:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 279 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :813:	
	ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT	50
30	GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA	100
30	GGCAAGGATG CTAACTCGAA GTCAATCACG CGAGTGATGT CATTCACAAC	150
	CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG	200
35	CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAA AGCTAGACGA	250

(2) INFORMATION FOR SEQ ID :814:

CTGACGAAAC CTGAGAACCC CGAAGGACT

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

5 .		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :814:	
10	AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC	50
10	ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA	100
	CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG	150
15	GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC	200
	AGCAGCCA	208
20	(2) INFORMATION FOR SEQ ID :815:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :815:	
	AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG	50
	CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG	100
35	TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC	150
	AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA	192
40	(2) INFORMATION FOR SEQ ID :816:	
70	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 264 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :816:	
	GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG	50
10	CCGCCTGGGG TAAGGTAGGC GCGCACAATG GCGAGTATGG TCGCAGAGGC	100
	CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA	150
15	CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG	200
	GTGCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC	250
20	GCGCTGTCCC CCTG	264 [.]
20	(2) INFORMATION FOR SEQ ID :817:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 202 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :817:	
	ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA	50
35	AAAACCACTC AACAAGCAAA CAACCCATCC TGTTTTCATA ACGTTATCGT	100
	AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA	150
•••	AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA	200
40		
	TG ··	202

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(2) INFOR	MATION	FOR	SEQ	ID	:818:
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(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 179 base pairs	
.5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :818:	
	AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA	50
15	TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA	100
	CTGTATAGTT TTTTTTAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC	150
20	CCCATAGGAT AGGTAATGAA CTTTTTGTT	179
	(2) INFORMATION FOR SEQ ID :819:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 260 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :819:	
	TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT	50
35	AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAAA AAGAATTTAA	100
	GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT	150
40	CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAACTG GATCAAGTTG	200

TACGCGGGTC CACGAAGTGA CAGACGAAAA ATGAACGCAA GCTGATGTAA

	ACGCATCACA	260
	(2) INFORMATION FOR SEQ ID :820:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 226 base pairs	,
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :820:	
15	ACTCGGCACT TTCTTAGAAT AGACAATTTG CAAAATGTCC ATCCCAGGTT	50
	CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG	100
20	TGAACTTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC	150
	ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC	200
	TTTCCGTAAC TGAGTTTGAT TTCTCC	226
25	(2) INFORMATION FOR SEQ ID :821:	,
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 197 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
25		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :821:	
	CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTTT TGGTTGTAAA	50
40	TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA	100
	CTCLLTCLLT CLCCCTTTTT CLTCCCLLC CLLCCLLC	150

	GTGATTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC	197
	(2) INFORMATION FOR SEQ ID :822:	·
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 304 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :822:	
15	GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG	50
	GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG	100
	GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT	150
20	TGCGCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT	200
	CACCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT	250
25	AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA	300
	CATG	304
	(2) INFORMATION FOR SEQ ID :823:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 197 base pairs	
*	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :823:	
40	GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG	50
	AAAAAMA imiaamaa	

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•	GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG	100
	CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG	150
5	GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG	197
	•	
	(2) INFORMATION FOR SEQ ID :824:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 281 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :824:	
20	AAAAACAATG TCATTTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA	50
	CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT	100
	GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA	150
25		
	GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTTCCTTA ATAGCAATGA	200
	TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCAG ACAGCAAGCG	250
	some ·	
30	TTTTCCCACA GGTCTCGACA CACAGAAGAT A	281
	·	
	(2) INFORMATION FOR SEQ ID :825:	
	-	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 312 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

(xi) SEQUENCE DESCRIPTION: SEQ ID :825:

	TATTAAATTT ACTAGAATGT TACAGTTACA AATTTGGTAA TGTTCTTTCT	50
	GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC	100
5	TTTTATTCAT GATAGAAAAA TAATTCCTGG CTTCATCTCA CAATTAACTA	150
	ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA	200
	TCAAAGTGAT TCTCCCAGGC CAAAAAATCA AATAAGAAGT TATATTTTAA	250
10	AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT	300
	CTACTAATTG GC	312
15	(2) INFORMATION FOR SEQ ID :826:	
	(i) SEOUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
•		
ŧ		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :826:	
	ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA	50
	GGGCAGGGAG GGGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA	100
30	TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCCC CCGGGTCTCA	150
	GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA	189
35	(2) INFORMATION FOR SEQ ID :827:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 232 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	• •	

•	(xi) SEQUENCE DESCRIPTION: SEQ ID :827:	•
	CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT	50
5	ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA	100
	AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT	150
10	TTAGAGATTA TTTTGTTGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT	200
	ATACACCGGC GGGATATTCA AGAGTGGCTA AG	232
15	(2) INFORMATION FOR SEQ ID :828:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 282 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
20	(0, 00000000000000000000000000000000000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :828:	
25	(,	
23	GGACATTGGA ACACTATACT CTATTATTGC GGTCGTGCCT AGCAGTCTCG	50
	CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTT	100
30	TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACTCTC	150
	TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT	200
35	CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA	250
	GTAATTACCC CATATCATAA AATGCGGGCG GG	282
	(2) INFORMATION FOR SEQ ID :829:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 230 base pairs	
	(B) TYPE: nucleic acid	

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :829: 50 CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA 100 10 AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCGCTTC AACGTGCTCA 150 200 AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC 15 230 TGGACATCGG CCCGCTCCCC ACAATGAAAT (2) INFORMATION FOR SEQ ID :830: (i) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: 226 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :830: TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA 50 30 GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG 100 GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA 150 35 TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT 200 226 CCTGAAGACG CAGACACACC TAACAA

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID :831:

418

(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
· 5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :831:	
10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTCCTT CTTTTCTACA GCCTGCAGTT CATTTAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT	200
٠	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247
20	(2) INFORMATION FOR SEQ ID :832:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 112 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :832:	
	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112
	(2) INFORMATION FOR SEQ ID :833:	
40	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 173 base pairs	
	(B) TYPE: nucleic acid	
	(5) 11151	

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(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :833:	
	AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA	50
10	ATGTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG	100
	CCTGAGTGCT TGTGGCCACC ACACAACAGA TGCGGCCTTC CTCTTCACTG	150
15	GCCCCTCGGC TGCTGCGG TCC	173
	(2) INFORMATION FOR SEQ ID :834:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 288 base pairs	•
20	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
23	(xi) SEQUENCE DESCRIPTION: SEQ ID :834:	
	TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT	50
30	TCCATCATTC TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTC	100
	CAGACTTATC TTATATTTTC ACTTCCCCAT ACCTGGAATC AATCACTTCT	150
35	CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC	200
	GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG	250
	AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT	288
40	(2) INFORMATION FOR SEQ ID :835:	

(i) SEQUENCE CHARACTERISTICS:

420

(A) LENGTH: 310 base pairs(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
,	(xi) SEQUENCE DESCRIPTION: SEQ ID :835:	
10	CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAAACCAG CAAGTTTTTA	150
15	TTAGTGATTT TAAAAGGGGA GGGAGTGTAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTTCACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	. 310
	(2) INFORMATION FOR SEQ ID :836:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 177 base pairs(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :836:	
	TCAGTGGAGG AATTAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	5
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	10
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTTA	15
	CATCTCCCAA AATGCCTAGC ATTCTTC	17

	(2) INFORMATION FOR SEQ ID :837:	•
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :837:	
	CCGTTGCACT TGGTGTTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC	50
15	CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA	100
	TGTTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT	135
20	(2) INFORMATION FOR SEQ ID :838:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 201 base pairs	
25	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :838:	
30	TCAGTGGAGG AATTAAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
35	GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTTA	150
	CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA	200
	G	201
40	(2) INFORMATION FOR SEQ ID :839:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 bas pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :839:	50
	TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA	30
	GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCTATA CACCCTGAGA	100
15.	TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT	150
	CTGAGATGTA CACGAACGAG ATCTTTTGAG A	181
20	(2) INFORMATION FOR SEQ ID :840:	
	(i) SEQUENCE CHARACTERISTICS:	
	(7; LENGTH: 222 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :840:	
30	CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG	50
	TTTTAGTGAA CATTCAGAGG AGTTTGGAAG AAAGTCGCTG CACAATCTTC	100
35	ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA	150
	TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA	200
40	TAATAACATG GGTTTAAAAA AC	222
-10	(2) INFORMATION FOR SEQ ID :841:	

5

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID :841:	
10	CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCCTTGCT CTTGCTGCGG	50
	CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC	100
15	GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCTGCT CACAACTCCC	150
	TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC	200
•	TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT	250
20	GTCATTGTTT TGGAACTTCT CCTTCAGCTT GGTCTTTTGC CGG	293
	(2) INFORMATION FOR SEQ ID :842:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 239 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :842:	
35	ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC	50
	TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTTT TGGCAGGTCA	100
	GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCAAA GACACAGG	150
40	AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC	200

	TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAAA	239
	(2) INFORMATION FOR SEQ ID :843:	
5	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 154 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :843:	
15	TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTC	50
	AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA	100
20	CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT	150
20	TGTC	154
	(2) INFORMATION FOR SEQ ID :844:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 392 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :844:	
35	GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG	50
	CCAGGAGTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC	100
40	TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC	150
	דבררדדבבאב כרדדאבליררר דרררדדאבבב ררררדראבר רדארררדאדר	200

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•	CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCACTAG CAGGTTCCCC	250
	ATCTTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTTCTGA AAAAATCTAG	300
5	ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG	350
	GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT	392
	(2) INFORMATION FOR SEQ ID :845:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 200 base pairs(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :845:	50
	GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTTGAGA AAGTGATATG	100
25	AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT	150
	GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA	200
30	(2) INFORMATION FOR SEQ ID :846:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 311 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :846:	

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA

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•	GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG	100
	AGGAGCGAGA TCTCCCCAAG CCTCCAGGAT TGCAGTCTGT TTTGTGCCTT	150
5	CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC	200
	AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC	. 250
	ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA	300
10	GAGGAGGTGG T	311
	(2) INFORMATION FOR SEQ ID :847:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 287 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :847:	
25	CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA	50
	CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC	100
30	GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC	150
	CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG	200
7.	GCAGCTCGAG GCCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG	250
35	CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT	287
	(2) INFORMATION FOR SEQ ID :848:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 263 base pairs	
40	(A) LENGTH: 263 base pairs (B) TYPE: nucleic acid	

427

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :848:	
	GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAAC	50
	TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA	100
10	TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG	150
	AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AAACTATACA	200
15	AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG	250
	AGGCATATNA CCA	263
20	(2) INFORMATION FOR SEQ ID :849:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 279 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :849:	
30	TTGTCAGTCA GAATAGGATG TAAAAGACTA TTTCAAAGAG TTAAATTATT	50
	TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG	100
35	CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT	150
	TGACATTAAA AACGAATGGA TACCCAACTC TGAATTCCAT ATCGTTTTTT	200
40	AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA	250
40	GTTTATCGAA ATCCTGCCGC TACTAAACA	279

(2) INFORMATION FOR SEQ ID :850:

(i) SEQUENCE CHARACTERISTICS:

•	(A) LENGTH: 173 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :850:	
	GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC	5
15	AGCATCTGGA TAAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT	10
	GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA	15
20	TGTTTATGAG CTCTCGACAG AAT	17
	(2) INFORMATION FOR SEQ ID :851:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 240 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :851:	
	TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA	5
35	TGGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG	10
	TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG	15
4.0	GGACTACAGC AACAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC	20

AGCAGGAATT TTCTGTTAAA AATATTTTTG CCGTAATACT

(2)	INFORMATION	FOR	SEQ	ID	:852:
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(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 314 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :852:	
	ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAATGTTA	50
15	AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACAACATCT	100
	GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC	150
20	CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA	200
	TTCCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC	250
	CCTCGAAATT TACTATTTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG	300
25	TCCTTGCCGT CACT	314
	(2) INFORMATION FOR SEQ ID :853:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 267 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :853:	
40	TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA	50
40	CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT	100

	ATTTCTTCAG TGACAAGCAA ACTATCCCCC CACATGCCTT TAATGGCCAG	150
	TGTTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA	200
5	CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC	250
	GCGCCAATAC TGCTTAA	267
	(2) INFORMATION FOR SEQ ID :854:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 186 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :854:	
20	GCAGTGGATC TTTCTTTTT TCCAAAGGAA ATTTCATATA GAGTCCATTC	50
	ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG	100
25	GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCCTAT AGGATGGCCA	150
	TTAGGTGAAG CAGTTTAGCT TGTTGGTTCA GACCTG	186
20	(2) INFORMATION FOR SEQ ID :855:	
30 .	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 162 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :855:	
40		-
	ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATTT CATAGTCAGC	50

	CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG	100
	GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT	150
5	GGCCCAAAAA TT	162
-	(2) INFORMATION FOR SEQ ID :856:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 286 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :856:	
20	TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA	50
20	GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT	100
	GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG	150
25	GAACAACCTG CCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC	200
	AACATAACAA ACCCAATCGC CCTGTTAACT TTAAATCTTC AACTCGAGAA	250
30	AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC	286
	(2) INFORMATION FOR SEQ ID :857:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 280 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

	AACTATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC	50
	GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT	100
5	CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG	150
	ATTTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC	200
10	TTTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT	250
10	CGGCGCCAAG GCCTTTACAT GAATACTCAG	280
	(2) INFORMATION FOR SEQ ID :858:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 310 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :858:	
25	CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG	50
	GCCAGGCTGG TCTTGAACTC CCAGCCAACC TCAAAGTGCT GGGATTACAG	100
30	CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC	150
30	CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTTACAT	200
	CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT	250
35	TATACAGGGC TTGAACTGTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG	300
	AGGCAGTAAC	310
40	(2) INFORMATION FOR SEQ ID :859:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs

433

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	·
•		
.5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :859:	
	•	
•	TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG	50
10		
	CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT	100
	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
	CCICIOCAGO ICANOCCAGO GCITOGO CACINCITCA TCINICOCOC	130
15	AGGAAGAG	158
10	ACCARONO	200
	(2) INFORMATION FOR SEQ ID :860:	
	2	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 263 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :860:	
	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
30	IIICIAAINA GAACAINAAA IRAAGGCIAA IIAAAAGAAG GIGACIGAGI	30
30	CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
	TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC	150
35	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG	250
	GAATAATGAG CCA	263
40		
	(2) INFORMATION FOR SEQ ID :861:	

(A) LENGTH: 254 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(i) SEQUENCE CHARACTERISTICS:

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :861:	
10	ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG	50
	GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAAACTG ATAAAAGATT	100
15	ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT	150
	TGATCCCATA GGTCATTTGT TATTACTCTT CTTCAACAGA GTGATTTTCT	200
20	ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG	250
20	AAAG	254
	(2) INFORMATION FOR SEQ ID :862:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3 base pairs (B) TYPE: nuc _c acid (C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :862:	
35	GTTCCTCCTT TGTAAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT	50
	GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC	100
40	CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGTCTGC	150
40	TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA	200

	TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC	250
	TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT	300
5	TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC	337
	(2) INFORMATION FOR SEQ ID :863:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 169 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :863:	
	TGGTGGGTTC GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC	50
20	GGTGCGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC	100
	TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA	150
25	ACTTACAATG CCACCGCGA	169
	(2) INFORMATION FOR SEQ ID :864:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 286 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :864:	
	ATTAAGGTAA AGGAAGACTT TCCATTGTTA AGTAGAAAGA GTGTCCTGCT	50
40	ATTACTACCA TTCACATCTA CTTTGTGA ACTAGGGTTT TCTATCTTAA	100

	CCCTGTTAAA AACAAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG	150
•	CGGATAGCAT TATCTTCCTG TGTTCCAGAC TGGAATGAAT TTATGAACAA	200
5	GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGTT TTCGTTTTTG	250
	CATTTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC	286
10	(2) INFORMATION FOR SEQ ID :865:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 272 base pairs	
	(B) TYPE: `nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :865:	
20		
	ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA	50
	·	
	GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG	100
		150
25	GCCTTGATTT CTGTCCCCCT TGCCTTGCGT GGCCTTTGAA TTGAAAGCTT	150
	TGAATTAGGC CTTCATAGAT TTTAGTGTGC ATACAAATAA CACGATCTTT	200
	IGANIIAGGC CIICAIAGAI IIIAGIGIGC AIAGIRRIAN GAGGAIGIII	200
	TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC	250
30		
	GCATTTCTGA TCTATAAGGT GA	272
		٠
	(2) INFORMATION FOR SEQ ID :866:	
35	(i) SEQUENCE CHARACTERISTICS:	
<i>33</i>	(A) LENGTH: 296 base pairs	
	(B) TYPE: nucleic acid	
-	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
40	\-\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	

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	(xi)	SEQUENCE	DESCRIPTION:	SEO	ID	:866
--	------	----------	--------------	-----	----	------

	ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAAACG GAACGCAAAT	50
5 ·	AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG	100
	GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG	150
	CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG	200
10	TTTCTAACAC TACAACGCTA ACTTTTGGAA CGTATCTACT TCTAGCATGT	250
	AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG	296
15	(2) INFORMATION FOR SEQ ID :867:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 241 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :867:	
	TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG	50
30 '.	CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA	100
30	CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT	150
	CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT	200
35	GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A	241
	(2) INFORMATION FOR SEQ ID :868:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 130 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :868:	
	GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC	50
·	ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT	100
10	CAAAGCCCAA TATAACCAAG GGGAAGGAAT	130
	(2) INFORMATION FOR SEQ ID :869:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 310 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :869:	
25	TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTTGAAAAA	50
	CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAAATTTAA	100
30	TTCARATGGT CARATTCCTG GARARCACAA ACTCCCTTCA CTARCAGAAT	150
30	TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA	200
	TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT	250
35	TCCCAAGCAC TTAAACAATA AACAATGCCC TCTTTATACA AACCTTTCCC	300
	AGTAATAGAA	31
40	(2) INFORMATION FOR SEQ ID :870:	
70	(i) SEQUENCÉ CHARACTERISTICS:	

(A) LENGTH: 192 base pairs

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(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :870: AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA 50 10 TTGGAGGAGC TGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC 100 CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG 150 15 CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG 192 (2) INFORMATION FOR SEQ ID :871: (i) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :871: ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG 50 30 AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT 100 TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA 150 35 CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA 200 TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA 250 (2) INFORMATION FOR SEQ ID :872: 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

440

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

	(b) TOPOLOGI: Timedi	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :872:	
	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
10	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
20	TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313
	(2) INFORMATION FOR SEQ ID :873:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :873:	
35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

	GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAAACT	250
	ATCCAGCGTT AGCACAAATG	270
. 5	(2) INFORMATION FOR SEQ ID :874:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 229 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :874:	
	TTGGGCCATG TCCCCATTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC	50
20	TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT	100
20	GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT	150
	TAATGACAGC TGATTATTTC CATCTGCAAA CTTACTCAAG AATGCAATCC	200
25	AGACTAACAC GACAATAGGA CATCAAGCT	229
	(2) INFORMATION FOR SEQ ID :875:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 294 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :875:	
	TTTGAACTTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC	50
40	CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT	. 100

50

442

	TGGTCTTGÄC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG	150
•	AAGGCTTTTG TGTTTCCCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA	200
.5	AGCACCGTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT	250
	ACACGGAACT GTCCTCGACC CGTGGGTAAC AGTATTTTCT GCGT	294
10	(2) INFORMATION FOR SEQ ID :876:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 173 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(wil epoliphop predpipmion, epolip .076.	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :876:	
	ATTTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG	50
٠	TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT	100
25	CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT	150
	ACGCCAACAA AAACCGTTAT TAA	173
	(2) INFORMATION FOR SEQ ID :877:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 143 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
J.J	(b) Torobodi. Ilmeat	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :877:	
40		

TAATCAAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAATGT

	CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATACTGA TAATATACTG	100
	AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTCG AAC	143
.5	(2) INFORMATION FOR SEQ ID :878:	
	(i) SEQUENCE CHARACTERISTICS:	٠
	(A) LENGTH: 213 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :878:	
	ACTGAATAAA CTGCTGATGT CCAGGTTCAG TGGTTCCTGC TGTGGGACTT	50
20	GCGTTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC	100
20	AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA	150
	GGGCTTCTAT TGCTAATGCC TGTAAACCTT GCTGAATCTA TAACAGAGTC	200
25	TATACCGCTC TCG	213
	(2) INFORMATION FOR SEQ ID :879:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 227 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :879:	
40	AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA	50
40	ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC	100

	CCTTCTTAGA ATGTGCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT	150
	AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC	200
5	TACCAGAGTA ACCGTCATCC CCTTGAG	227
	(2) INFORMATION FOR SEQ ID :880:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 221 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :880:	
20	ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG	50
20	AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT	100
	TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA	150
25	TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA	200
-	ATAATCACTC TTTACAAGGT A	221
30	(2) INFORMATION FOR SEQ ID :881:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 310 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :881:	
40	>> mmcmccom> m>mmmc>mmm >>>>mmcc>mc >>>c>c>c>c> >c>c>c>c	E 0

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	ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT	100
	CATATTAAAA CAATGATAAG TAATACTTAG AAACTGCATC CTAGAGACAC	150
5	ATCATTCGCA TTTTTAGAAA AACAGAAACA TATTAGTGTG AAAAGATGTT	200
	AAAAAATGAA TATTAAACCG TCGAGCACAA CACACTACGC CGATAACAAT	250
10	ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT	300
10	GGCGATCCGA	310
	(2) INFORMATION FOR SEQ ID :882:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 177 base pairs(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :882:	
25	GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT	50
	GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACAC CACACACATA	100
30	CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA	150
30	CGAACTACAA ACGTAACAGC AGCAGGC	177
	(2) INFORMATION FOR SEQ ID :883:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 152 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	

•	(xi) SEQUENCE DESCRIPTION: SEQ ID :883:	
	CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCCTCTGA AGATACACGT	50
5	ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA	100
	ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC	150
	GA	152
10	(2) INFORMATION FOR SEQ ID :884:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 177 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :884:	
	CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT	50
25	GACCTATTTC AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT	100
	ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA	150
20	AAATGAAATT GTGCCGAAAT GTATACA	177
30	(2) INFORMATION FOR SEQ ID :885:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 241 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
*		
40		

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(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

	CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT	. 50
	TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAACTAGAA	100
. 5	TTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT	150
	GTAACATATT TAGACATAGT ATATATATA ACAAGTGTAA CAAATATATA	200
	TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A	241
10	(2) INFORMATION FOR SEQ ID :886:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 190 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :886:	
	GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAACTCG ACAAGTAACA	50
25	ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA	100
	ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG	150
20	CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAACA	190
30	(2) INFORMATION FOR SEQ ID :887:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
•	(D) TOPOLOGY: linear	
40	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :887:	

•	CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA	50
	CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA	100
5	CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA	150
	CTATAATATT ATACTCTC	168
	(2) INFORMATION FOR SEQ ID :888:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(1) SEQUENCE CHARACTER STICS. (A) LENGTH: 174 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :888:	
20		
	ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT	50
	GCCGATCTCG CAACCGGTTC CAGTTAGACA GAACATTGTG ATATTCAAAC	100
25	CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT	150
	AATCATATTC TAGTCCACTG TAGC	174
	(2) INFORMATION FOR SEQ ID :889:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 327 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :889:	
40	ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA	50

	TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATA	100
	TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT	150
5	ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA	200
	AATCTCCCAT GGCAGAGAG TATCCCAAAA AATTTTTTTG TGTGTAACAA	250
10	AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT	300
10	ATATATAT CTGTATATAC AGGTATA	327
	(2) INFORMATION FOR SEQ ID :890:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 181 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :890:	
25	TTTTTTTTTT GTCTCTCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC	50
	GCTCTCTCC GCTCTCCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC	100
30	TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT	150
	ATCTCCTCGC GCGCGCCCG AGCGCCCCC T	181
	(2) INFORMATION FOR SEQ ID :891:	
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 207 base pairs	
a.	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :891:	
	CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC	50
5	TCTCAGGGGA GGGAGGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT	100
	TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA	150
10	TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG	200
10	CAAAGAA	207
	(2) INFORMATION FOR SEQ ID :892:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 198 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(b) Torobott. Ithicar	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :892:	
25	CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG	50
	TGATTTTACA GTAGAGTGAA CGAAACTTGG GAAGGAAAAC ATCCAAGAGG	100
30	CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT	150
	TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAAACACTC TCTACTCT	198
	(2) INFORMATION FOR SEQ ID :893:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 96 base pairs 	
·	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(x1) SEQUENCE DESCRIPTION: SEQ ID :893:	
	CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT	50
5	TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG	96
	(2) INFORMATION FOR SEQ ID :894:	
1 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :894:	
20	AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA	50
	ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTTG TCGGCGTGGT	100
	GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA	150
25	GAGTGAGCGT GGGAGGGTGT GGTCGGTGGA GAGGTGAGTG	200
	TGCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG	250
30	GACAAAATAT ATATATATA AGATATAATA GATATGAGAG AACACTAAAC AATAACCACT ACTCACATAG AATAT	300
	(2) INFORMATION FOR SEQ ID :895:	323
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

		-
	(xi) SEQUENCE DESCRIPTION: SEQ ID :895:	
	ATAGTTGTAC ATTTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC	50
5	AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA	100
	TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT	150
10	TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTTGTGAAT	200
10	AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTTGAT ATACTGATTT	250
	TCTTTCTTTT GTTATA	266
15	(2) INFORMATION FOR SEQ ID :896:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 197 base pairs(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	·
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :896:	
	AAGAAGAGTC TTCTGCACAA ACAAAACCAT AGTGTTGACA AATAGTCATG	50
30	GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG	100
	GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT	150
	AGCAGGCCCA GAAGACCGCC CCGCCCCCCA TGCCCTGGCG CAGGGCC	197
35	(2) INFORMATION FOR SEQ ID :897:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 192 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :897:	
	GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT	50
5	GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTTGTGAA	100
	TATTTTTCTT CCGACTAACT CGCGCCCCAC TCTCTTGCGA GCACAAACAC	150
10	ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT	192
	(2) INFORMATION FOR SEQ ID :898:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 224 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :898:	
25	TGGATGTTTT CATTCGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC	50
23	TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG	100
	AATGGGCGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT	150
30	ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT	200
	GCTCTAGTAG CCCACAGCCC AATC	224
35	(2) INFORMATION FOR SEQ ID :899:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 362 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

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/ v i \	SECUENCE	DESCRIPTION:	SEU	תנ	: 677:	

	(XI) BEGOLNED BEGOLITIES AND ALLE	
	GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCAAAAT ATTCTAATGT TTCAATGTTC TACATGAACA TATAGGGAAG	150
10	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
10	CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTTGTCAAA TTATAAAGAT	250
	ATATTCCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTTCCT CTCGAGAATT GTGAAGGTTC	350
	TGAGATTTGA TT	362
20	(2) INFORMATION FOR SEQ ID :900:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 310 base pairs	
	(B) TYPE: nucleic acid	
*	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :900:	
30	GTATGTAGCC CAGTGGGTGT CTTCCCACAG GGTAGGTACT CAGTTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAGTGCA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250

AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTTGGT

	TTCTCGATGA	310
	(2) INFORMATION FOR SEQ ID :901:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 185 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :901:	
15	TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA	50
	CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA	100
20	GGGGGCGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC	150
20	CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA	185
	(2) INFORMATION FOR SEQ ID :902:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 381 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :902:	
35	ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG	50
	TCAAACAACT AAACTACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA	100
40	GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA	150
40		200

	AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAACTCCTG TAAAGAGTAA	250
	GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT	300
5	TGCCTTCAGA AACACTTTGC CTTTTAATAT GTGTAGCTAC AGTAAGTACC	350
	AATGGGCTAA CTAATTGAAG CTAACATTTT A	381
	(2) INFORMATION FOR SEQ ID :903:	
10	(i) SEQUENCE CHARACTERISTICS:	
	• • -	
	(A) LENGTH: 240 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
00	(xi) SEQUENCE DESCRIPTION: SEQ ID :903:	
20	CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAAACTG ACATATGTAT	50
	ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC	100
25	CTCTGCGCTG TTGCGGGTCC TGCGGAAGTC CTCGGAGCGG CCGTCGCGGA	150
	AAGCTCGGCA AAGAGAGGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC	200
30	ACTITITIT TATCGGCACC AGGCCGCGTC CTCCTCCC	240
	(2) INFORMATION FOR SEQ ID :904:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 280 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(2,	

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(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

	CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG	50
	TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCCTAAGG	100
5	TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG	150
	CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA	200
10	CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG	250
10	TGCTGGTCTG TGTGCTGGCC CATCACTTTG	280
	(2) INFORMATION FOR SEQ ID :905:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 225 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :905:	
25	GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT	50
	AAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT	100
30	ATTTGCACGA GTAAAGCGTA GCAAGTTTAA CACAACTTAT GTAAACTTGG	150
50	AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA	200
	TACACATCTC TCATGCACAC ACGCG	225
35	(2) INFORMATION FOR SEQ ID :906:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 161 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :906:	
	GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA	50
5.	ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA	100
	TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG	150
10	TCCACTGTAG C	161
	(2) INFORMATION FOR SEQ ID :907:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 204 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :907:	
	AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAAT	50
25	ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT	100
	TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT	150
30	TATATATGCG CACACACA CACACACGAC ACGACGACAC ACACACAC	200
	тста	204
	(2) INFORMATION FOR SEQ ID :908:	
35		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 316 base pairs	•
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

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	CHOURNOR	DESCRIPTION:	CEO	TD	.000.
(XT) SEGRENCE	DESCRIPTION.	350	10	. ,

AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA 50 AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC 5 100 TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC 150 ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA 200 10 CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA 250 CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC 300 CAAATGTGTG TGTTTT 316 15 (2) INFORMATION FOR SEQ ID :909: (i) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :909: CTAGTAACAT AGAAAATAAA CTTCAGTGGG AATCTCTGCT TCCCGCGTGA 50 30 GGTGTTTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT 150 CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAAACTG GATCCCACCA 35 CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA 200 TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG 250 GGAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTAA 300 40

GCTATTT

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(2) INFORMATION FOR SEQ ID :910:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 172 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :910:	
	TTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTTGCTC AATCAAACGC	50
15	AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT	100
	TANACCGAAT CCCCACAATC TCAAACTCAA CCAGGCCAAA GGGAACACAG	150
20	TGACACAACA ACAGGGTTCC AA	172
20	(2) INFORMATION FOR SEQ ID :911:	
25 _.	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 255 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :911:	
	GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA	50
35	CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG	100
	AGAGATAGAG AGAGATACAC ATACACACT TCATCAACGA GAGAGAAGAG	150
4.0	AGGAAAGAGA GAGAGGGA GCACAGACAG AGATAGAGCA CACAGAGAGA	200
40	TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG	250

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	CATCT	255
	(2) INFORMATION FOR SEQ ID :912:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 196 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :912:	
		-
15	CAAGCGAATG GTAATTACAT GGTCGGATGA GGTCCTCACT CTCAGGGGAG	50
	GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT	100
20	GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT	150
	GCAATTTACA AGAGATTTCT TTGAAAGAAA ATAGGAAGGC AAAGAA	196
	(2) INFORMATION FOR SEQ ID :913:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 203 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :913:	
35	ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA	50
	GCGATTTTAC AGTAGAGTGA ACGAAACTNG AGAAGGAAAA CATCCAAGAG	100
	GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA	150
40	TCCCACTAGG GCCACGAGAA ACAAAGCAAA TTAAAACATT ATCCACTACA	200

	CGA	203
	(2) INFORMATION FOR SEQ ID :914:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 262 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :914:	
15	CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCCC ACCCGGGCAA	50
	GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT	100
20	AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTTG AAAATAAATC	150
20	TTAGTGTTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAAATCGGA	200
	TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG	250
25	GAGGTGGACA TT	262
	(2) INFORMATION FOR SEQ ID :915:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 191 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :915:	
·		
40	TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT	50
	ACACCCACTO TOTATTTTOO ATCOTAGAAT CATTAACCAG AAACAAAGAA	100

	AGGAAAAAGG TAAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT	150
	AAAGAATGAA ATAATTTGAA AAAAAAGGCA GGGCAGGCAA A	191
5	(2) INFORMATION FOR SEQ ID :916:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 252 base pairs	
	(B) TYPE: nucleic acid	•
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		•
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :916:	•
	AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT	50
	TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT	100
20	GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC	150
	AGTGTGTGCA TATGTTTGTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT	200
25	CTCCCCCTCT GTCTCTCC AGAGATATGT GTGGCGTCAC TGTACTCTTG	250
	TG	252
30	(2) INFORMATION FOR SEQ ID :917:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 247 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :917:	
4 0	TACACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAAGGA	50

	GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT	100
	TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC	150
5	ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT	200
	CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC	247
	(2) INFORMATION FOR SEQ ID :918:	
10		
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	• •	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :918:	
20	(XI) SEQUENCE DESCRIPTION. DEG 15 (910)	
20	ATTTGGATTC AATTGCCTGT TGCACTTTTA CATTAAGTGT TGCTTAAATA	50
		100
	AACAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG	100
25	CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT	150
	TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T	191
	(2) INFORMATION FOR SEQ ID :919:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 205 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :919:	
40		
	CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAAAAA	50

	ACAACCTCCT CATTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG	100
	ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT	150
5	CGAACAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC	200
	AACCC	205
	(2) INFORMATION FOR SEQ ID :920:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 323 base pairs	
	(B) TYPE: nucleic acid	
,	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
·	(xi) SEQUENCE DESCRIPTION: SEQ ID :920:	
20	·	•
	GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTTCCTC TCCAACGACT	50
	·	
	CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA	100
25	CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA	150
25	CATCTCCTAT CGTTAGTTGA ATMAATTCAC ACACCGCGTT TAAGAGATGA	150
	AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT	200
	TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA	250
30		
	AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG	300
	CTCTAAGCTA CAGGTTGATC ATA	323
35	(2) INFORMATION FOR SEQ ID :921:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 230 base pairs	
40	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

•	(xi) SEQUENCE DESCRIPTION: SEQ ID :921:	
	AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA	50
5	GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG	100
	ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG	150
10	GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC	200
	TATAGAAACA ACAAGTTAGA GTACAGACGT	230
	(2) INFORMATION FOR SEQ ID :922:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 239 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :922:	
25	TATTTTCCT GATGTTCTCC CTTCCTCCAG TCCCCGACCT CCCACAGGCC	50
	CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTCAG	100
30	TGCCCATTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC	150
	TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC	200
25	TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTTGTAA	239
35	(2) INFORMATION FOR SEQ ID :923:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	·

	(xi) SEQUENCE DESCRIPTION: SEQ 1D :923:	
5	GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT	50
	TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT	100
• •	TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC	150
10	TGAAACCCGT CCACTCAATA AATTTTTG	178
	(2) INFORMATION FOR SEQ ID :924:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 325 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	·
20	(b) TOPOLOGI. Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :924:	
25	CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG	50
	ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC	100
30	AAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT	150
	TCTTGCTTCT TGTTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA	200
	GCAATCTCAT GGTTCTTGGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA	250
35	GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTTCTGGC CTATTCATTT	300
	ATTTTTGGGG GATGAATTTA CAGTA	325
40	(2) INFORMATION FOR SEQ ID :925:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 261 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :925:	
	ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG	50
10	AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT	100
	CCGGTTTTCT TTGTTTTTTC TCTTTATTCG TCCTTTCTCA AAGATGGGAT	150
15	ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG	200
	AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG	250
20	TTCCAGTCCT G	261
20	(2) INFORMATION FOR SEQ ID :926:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 173 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :926:	
	GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC	5
35	AACTGGGTTC AAATCCTGGC TCTGTCACAT ACTAGCTGTG TGACCTTGGC	10
	CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT	15
40	AACCAACCAA GAGAGCTGAG AGA	17
40	(2) INFORMATION FOR SEQ ID :927:	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :927:	
10	AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC	50
	CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TGCGCCATCC	100
15	TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC	150
	CTTNGATTTT TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC	200
	TCAGATCATT ACTACTGAAC TCG	223
20	(2) INFORMATION FOR SEQ ID :928:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 212 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :928:	
	GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT	50
35	ATTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA	10
	CCACAGATTA AGTGAAGACA CCCACAACTT TAATGACTCT ACGACTCTCG	15
	GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT	20
40	CATAACTTGC AT	21

200

40

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	(2) INFORMATION FOR SEQ ID :929:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :929:	
	TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT	50
15	ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT	100
	TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG	150
20	TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG	200
20	ACATAACTTG AGTTTGTTTG CTTGGTATTT ATT	233
	(2) INFORMATION FOR SEQ ID :930:	-
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :930:	
35	AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA	50
-	GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC	100
	AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA	150

GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC

	TCCCACCCC CCCAGGCATT CAGCACCCGC AAAAG	235
	(2) INFORMATION FOR SEQ ID :931:	
, 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 221 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :931:	
15	CTATCTAGAA TTACTTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT	50
	TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGA ATAATGGCAT	100
20	CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA	150
	AAACAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC	200
	ACACACAC ACAAAAACA C	221
25	(2) INFORMATION FOR SEQ ID :932:	
	'(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 333 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :932:	
	TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATAT ATGTCTTGAG	50
40	CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC	100
40 .	TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA	150

	TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG	200
	GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA	250
.5	ACGGAGCAGG TCAAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT	300
	GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA	333
10	(2) INFORMATION FOR SEQ ID :933:	
10	(i) SEQUENCE CHARACTERISTICS:	
	• • -	
	(A) LENGTH: 281 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
15	(b) TOPOLOGI: Timear	
		*
	(xi) SEQUENCE DESCRIPTION: SEQ ID :933:	
20	(,	
	AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA	50
	GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT	100
•		•
25	TGTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTTCTG AATGTTTAAG	150
	AAAAAAÁTAA TACTTTTCAG AATTACCTAC CTCTTTCTCA TTTTTAGCCT	200
	GGGATCAATT ATTCCCTTTC ACACTTTTTT ACATCCTAAG TAGAAATAAA	250
30		
	ACTCTTTATT CTATTTTTT TCAGTTATTG G	281
	(2) INFORMATION FOR SEQ ID :934:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 266 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	•	

•	(xi) SEQUENCE DESCRIPTION: SEQ ID :934:	
	AATCTTGTAT TATGTTAATA TTAAAATCTA ATAATAAGAT ACTGTAGAAG	50
5	TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG	100
	TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAAACTGTT	150
10	GTTTTATCCC AAGGGTAGAG GGACTCTAAG TAAAACTGTA ACAGAATCAA	200
10	AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAACT	250
	TTAAATAAGT AAATCT	266
15	(2) INFORMATION FOR SEQ ID :935:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 178 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID :935:	
	GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAACT	50
30	ACTANTANCT CATTANATAN ATTANTANTA TTANATGATC TGTGTGTTCC	100
30	ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA	150
	TTACTCTAAC ACCAATAACA ACACGTAA	178
35	(2) INFORMATION FOR SEQ ID :936:	
·	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 224 base pairs(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :936:	
·5	ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGA CACCAGAGGC	50
	TCCTCCATGA GCAGCAGGAG TGAGCGAGG AATGTGCCCC ACAGCAACTT	100
	TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG	150
10	AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGCTGAAAGTTAG	200
	ACTTCACCCG AATTACATTT ACCA	224
15	(2) INFORMATION FOR SEQ ID :937:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 270 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :937:	
25		
	ATTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT	50
	GGGGATGGGT AGAGAAAACC CATTTATAGT ACTTTTCTGC CTTCTTGTGG	100
30	TTTTCGGCTT TGCGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAA	150
		200
	AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTTCCAA	200
	CCAAAACTCC TAAAAAACCC AAAAACAGAA CAACCAATTA AACCCGACCC	250
35	GACACAACTA CCAATGACTG	270
	(2) INFORMATION FOR SEQ ID :938:	
40	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 215 bas pairs	
	(B) TYPE: nucleic acid	
	(D) IIID. HOTCED WORK	

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(C) STRANDEDNESS: double (D) TOPOLOGY: linear

	·	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID :938:	
^	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
15	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
13	CTAGAACTAA AGTCA	215
•	(2) INFORMATION FOR SEQ ID :939:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 303 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :939:	
30	TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC	100
35	TTTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT	150
	ACCTTCATGA TTGCTTTTTA TTATTTCTTT CACTCATCAT TATTGTTCAT	200
	TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TGCGCTTTCT CAACCCCCT CCTTCCTCAT	300

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	(2) INFORMATION FOR SEQ ID :940:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs	
5	(B) TYPE: nucleic acid	
J	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :940:	
	(X1) SEQUENCE DESCRIPTION. SEQ 15 .540.	
	ACACTATTTT CAAAAATCCA AATAAAAGTG CAGTTTCAGA CTTTTTAAAA	50
15	AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG	100
	CGTTTGCATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT	150
20	TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT	200
	CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTŢCAGTT	250
	TGCTTTGCTT TGTGGAGACT TGCGCGTATT TTCTTTTGCT TGTTTGTTTA	300
25	TCGCCAGGCA GCGCTGTTCG AACTGTGAGA	330
	(2) INFORMATION FOR SEQ ID :941:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 107 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :941:	
	TTTATTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT	50
40		

TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT

	TTTTGCT	107
	(2) INFORMATION FOR SEQ ID :942:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 126 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :942:	
15	CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT	50
	GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT	100
	TTCGGCGTTA CACCTCCGGT GTTCTC	126
20	(2) INFORMATION FOR SEQ ID :943:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 155 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		٠
30	(with openings propriession, SEC ID .042.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :943:	,
	ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA	50
35	AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA	100
	GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA	150
	AGCTC	155
40	(2) INFORMATION FOR SEQ ID :944:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :944:	
10	CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT	50
	TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG	100
15	GGGGGGGTT TGGAAGCAAA CACATTTGGG GTTTTTAACC AATTGTTAGG	150
	TTCTTTTAT TTAGGGTTGT GCAGGGAACT GTTGGGAGGT TTCTTTAGGT	200
	GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT	250
20	TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG	287
	(2) INFORMATION FOR SEQ ID :945:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 149 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :945:	
35	ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG	. 50
	TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG	10
	GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT	14
40	(2) INFORMATION FOR SEQ ID :946:	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :946:	
10	TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTTAAATA	50
	AATTTCACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG	100
15	AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC	150
	ATTAACATTG GAAAACTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA	200
20	GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTTT	250
	TTTTTTCCC C	261
-	(2) INFORMATION FOR SEQ ID :947:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :947:	
35	CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACTCTG	50
	CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAAGTTG CACTATTGCA	100
40	AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG	150
	TCCTGTACCA GAAACATTTT CTTTTATTGT TACTTGCTTT TTACACTTTG	200

	TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC	250
	CAAGTTGTAT ATTT	264
5	(2) INFORMATION FOR SEQ ID :948:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 149 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :948:	
	CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA	50
20	GCCAGGTTGA TTGAGCACTG GGCTCCAACT TATTGTTAAT GAGAAACGGC	100
20	CCAACTTGGA CCATGACTTT CCCATTTGCA GGTCTTAGAA TAATTTTTT	149
	(2) INFORMATION FOR SEQ ID :949:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 242 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :949:	
35	CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA	50
•	GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA	100
40	GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG	150
40	TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTTG GCACCTTCCC	200

	CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT	242
	(2) INFORMATION FOR SEQ ID :950:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 153 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :950:	
15	ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG	50
	CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC	100
20	AAAGTTTATA CATGAAAATT TAAAAAGGGA GTCTATGCAA AGCGGAGTTC	150
	AGG	153
٠	(2) INFORMATION FOR SEQ ID :951:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 128 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :951:	
35	TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG	50
	TTGTTCCTAA GGCGAGCTCA GGGAGGATAC AGAAAACTCT CCTGTGGTGC	100
40	TATGAAATGT GGCGTAAAAA GCATTCTG	128
	(2) INFORMATION FOR SEQ ID :952:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs(B) TYPE: nucleic acid

•	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :952:	
10	GTTGGAAATT TCCC TAAAT CACCTACCGA TTACCCTTGA TTTCCCTTTG	50
	TTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC	100
15	ATATAAAAT AAAGTGTACC CAAATATTGT AATGTATATT GCTGCTCTTC	150
	TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC	200
20	AATTGATACA AAT	213
20	(2) INFORMATION FOR SEQ ID :953:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 236 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30 ·		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :953:	
	GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC	5
35	TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT	10
	TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC	15
	CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT	20
40	GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT	23

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(2) INFORMATION FOR SEQ ID :954:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 217 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(2, 20102011)	•
10		
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :954:	
	GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC	50
15	TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT	100
	TCATTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC	150
20	CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT	200
	GCCACTGCAG AAAGTGT	217
	(2) INFORMATION FOR SEQ ID :955:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 256 base pairs	:
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	·	
· ·	(xi) SEQUENCE DESCRIPTION: SEQ ID :955:	
35	AGCAGCGACC GCGCTCACTG GCTTTTTGTT TCTGCTTGGG CCTTTTCTGT	50
	TCAGTCCATG CTTGAACTAC TCCACCCCT TAAATCCAAC GTAAAAACCA	100
40	GTCTTTTCTG TGCTTGTTCT CTGTGCGTTA ATGCTTTTC TTATGCTTGC	150
40	TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG	200

	TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA	250
	TGCTTG	256
.5	(2) INFORMATION FOR SEQ ID :956:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 194 base pairs	
•	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :956:	
	CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC	50
	ATTTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT	100
20	AATTTTTAAA AATAACATTA AAAAATTTTT TAAAATGTGA ATATACCACA	150
	ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA	194
25	(2) INFORMATION FOR SEQ ID :957:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 196 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :957:	
	ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT	100
40	CATTTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGAG	150

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	GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA	196
	(2) INFORMATION FOR SEQ ID :958:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 105 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(b) TOPOLOGI: Tillear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :958:	
15	GCGCTCAGCT GGAACTTCCG ATCTATTTTT TCTTGGTCTC ATACTCAGTT	50
	TTTTTATGTA GTCACTTAGT AAAATAAACC TAAAAAAAAA CATTGATTTT	100
	TTCTG	105
20		
	(2) INFORMATION FOR SEQ ID :959:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 261 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :959:	
	GACAGCGACC GACACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA	50
35	GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA	100
	TAATTCATTA ACACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT	150
	TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC	200
40	TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG	250

	CTTTTGTTAA A	261
	(2) INFORMATION FOR SEQ ID :960:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 188 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :960:	
15	CACAGTTTTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA	50
	TCGTTTCTTC TTTAGAGGAG TAGGTTTTAA CCATGTTAAA TTTCCAAGAA	100
20	TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTCA GGAAAATAAA	150
	TAATTTTCGA TTCAAGTACT ATACAAACTT AACGATGG	188
	(2) INFORMATION FOR SEQ ID :961:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 191 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :961:	
35	ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC	50
	TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA	100
40	CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTTCT	150
-	ACABCCAAAA ACCCAGAGAC AAACCTGACC TAAAGCGCTC C	191

	(2) INFORMATION FOR SEQ ID :962:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 191 base pairs	
. 5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	••
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :962:	
	CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT	50
15	ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA	100
	TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC	150
20	CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAAT T	191
	(2) INFORMATION FOR SEQ ID :963:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
25 .	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :963:	
	AGCAGGCCAA AAGCCCAGGT GAGGCCCAGC AGGAACAGCA GCCCAATGCC	50
35	TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACACTTGA	100
	GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC	150
40	CGAACACCAT CAATAACCGA ATAGACTA	178
	(2) INFORMATION FOR SEQ ID :964:	

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(i) SEQUENCE CHARACTEPISTICS:

(A) LENGTH: 199 base pairs(B) TYPE: nucleic acid

-	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(b) Torobodi. Timedi	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :964:	
10	ACTITGCAGI CCICACATCA CAAATAGAGI AAAAGATICC CAAAAGGAAG	50
	GGGATCCTTT TGACTGCCAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA	100
15	TATCCTTTTA AACACACAC TCGACACAT TTTCCACTCT GCTAAGGGAT	150
	CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC	199
20	(2) INFORMATION FOR SEQ ID :965:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :965:	
30		- -
	ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTTT	50
	GGCACATCTG CCAAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG	100
35	ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT	150
-	CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA	200
40	ACCTGCAGGT TGGGGCT	217
	(2) INFORMATION FOR SEQ ID :966:	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs(B) TYPE: nucleic acid

•	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :966:	
10	(,	
	ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTCC	50
	AATTTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT	100
15	CAAGAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC	150
13	· ·	244
	TCATCAATAA AACGCAACAC TATCA	175
	(2) INFORMATION FOR SEQ ID :967:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 92 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
		•
	and the contract of the contra	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :967:	
30	AGGGGTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG	50
	GGGGACAAGG AAAACCTGGC GCCCCCCACC GCGAAAAACA CA	92
		•
35	(2) INFORMATION FOR SEQ ID :968:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 208 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :968:	
	GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA	50
5	TATTGTTCAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT	100
	ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AAACTCGAAC	150
10	AAATAACCGA AAACTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA	200
	CTACTAAC	208
•-	(2) INFORMATION FOR SEQ ID :969:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 256 base pairs(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :969:	
	AGTGGTTGGT GTTTACTGGA ATCTTGTTTT TTTTTTTTCG GTTTTTTTGA	50
	CTACTCGGGG GGTTTTCCTT TTTTACAGGA ACTAAATCAA CAAACTTTTT	100
30	CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC	150
	TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC	200
35	CACCAAGGAT TTACTCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT	250
35	TTAAGA	256
	(2) INFORMATION FOR SEQ ID :970:	
40	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 240 base pairs (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double (D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :970:	
	(XI) BEGOTAGE PERGITTEENS FOR ITS TO STATE	
	AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA	50
10	AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT	100
	CATTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA AACAATGCCT CTATTCCTTC AAGTATAATA	200
15	ANTGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240
	(2) INFORMATION FOR SEQ ID :971:	
20	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 184 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :971:	
30	ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TGCGCGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT	184
	(2) INFORMATION FOR SEQ ID :972:	
40	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 234 base pairs	
	(B) TYPE: nucleic acid	
	/=/	

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(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID :972:	
	GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA	50
10	TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTTA	100
	CATAATCCAG TGAAAACTCT ACTTGTTGAA ATTATGACAT AAAGATCTTG	. 150
	CAGCTTTATT TGAGTATTTG TTCTTTTGTG TAGTTTCCAT CTTTTAAAAT	200
15	ATTTAAAATA TTTTCAAGGA TAAAAGTATT ATCT	234
	(2) INFORMATION FOR SEQ ID :973:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 197 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :973:	-
30	TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC	5
	TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	10
25	AAAAAAACAT CACAAAACTG AACTGCCGCC ATCACCACTA CACCAAGTAT	15
35	GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC	19
•	(2) INFORMATION FOR SEQ ID :974:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 244 base pairs (B) TYPE: nucleic acid	

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

	•	
5 .	(xi) SEQUENCE DESCRIPTION: SEQ ID :974:	
•	AGCAGGAGAT TTTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAC AGGATCAAAG GAGCAACATA TCCAGTGACT TAAAAAAATA	100
	ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC	150
15	ATACAGAAAA AAACGAAATA CATACACCCC CAGGTTTGAA AGAAAATAAT	200
13	TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC	244
	(2) INFORMATION FOR SEQ ID :975:	-
20 .	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 330 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :975:	
30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG	100
35	AGACCCATTA GAGATTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA	200
·	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300

ATGTGCAATG AAGGGTTTCG TGTAATATTG

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(2) INFORMATION FOR SEQ ID :976:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :976:	
	TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT	50
15	TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT	100
	TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT	150
	AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA	200
20	(2) INFORMATION FOR SEQ ID :977:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 296 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :977:	
	AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT	50
35	ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT	100
	AATGATGTTA TGAAACGAGC TTTGCT 3 GCTCTTGATT GGAGCTTCCG	150
	GTATGTGATG ACGGTATGTS ATGTATGCAT GGATGTAC. S AACTGTGTTT	200
40	AATACTCTGA ATTTTAATTA GAAAAATA CAATAGCAGC AAGGCCCTGG	250

	TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC	296
	(2) INFORMATION FOR SEQ ID :978:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 228 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :978:	
15	GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG	. 50
	ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT	100
20	AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAGC CGGGGGAGGA	150
20	CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC	200
	CAGCCACTAC TGATAATTCA CAACGGTA	228
25	(2) INFORMATION FOR SEQ ID :979:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 171 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :979:	
	CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT	50
	CCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA	100
.40	AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA	150

	CCAGGCAAAA CCAGAACCTG A	171
	(2) INFORMATION FOR SEQ ID :980:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 241 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :980:	
15	TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC	50
	CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC	100
20	CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG	150
	ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATTA	200
	CTGCAGTGGA AAATAACTGC ACTCTCAGGA CACAGCACTG T	241
25	(2) INFORMATION FOR SEQ ID :981:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 227 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :981:	·
	TCACTGCAAT CACGGTAGCT TCGCCCATTG CCTCTTCAAC CAGGCACATA	50
40	CATCGAGAAG TTGAACCTGC ACTTTATTTC ACACTGAACA GACTTACCCC	100

	TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AAACATTTGC	200
	AAAACCACAC TTCAACCCAC AGGAAGA	227
5	(2) INFORMATION FOR SEQ ID :982:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 205 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :982:	
	CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG	50
20	ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT	100
	CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA	150
	CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC	200
25	AAAAG	205
	(2) INFORMATION FOR SEQ ID :983:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 204 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :983:	
	_ ·	
	AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT	50
40 .	TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT	100

	CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA	150
	CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC	200
5	CCCT	204
	(2) INFORMATION FOR SEQ ID :984:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :984:	
20	ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTTG CATTCTTGTT	50
20	TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT	100
	AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTTGCT TTTTTTTTC	150
25.	TTTCTCCCC CTCCCAG	168
	(2) INFORMATION FOR SEQ ID :985:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 350 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :98	
40	CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAL AGAAGCATGG	50
40	GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT	100

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	TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCA TCTCCAGGCG	150
	CTGGGAGGG GGCCCTCACC CCGTCACGCC TCGCTCCTC CTGGCCCTCT	200
5	GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT	250
	CCTGATGTAT TTTTTTTCC TCCAACTCAA AAGGCAAAAA TAATCCTATT	300
	TTTATTATCT TGCTACAACT GCAACTTTCT GCCCTATAAA TTTACATTCC	350
10	(2) INFORMATION FOR SEQ ID :986:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 289 base pairs (B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	A CARAMETER DESCRIPTION GEO. ID . OOC.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :986:	
	AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAGGTG AGCCGCTCTT	50
25	CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT	100
	TCAACAATGC TCTGCAAATC TTTTTAAGAC CCGTTACTTC AACAACTCCC	150
	AATACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA	200
30	CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA	250
	AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA	289
35	(2) INFORMATION FOR SEQ ID :987:	
,	(i) SEQUENCE CHARACTERISTICS:	
,	(A) LENGTH: 134 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :987:	
	CACAATCATA GCATTTATTA CACGATTTAC ATCTGATCCT CACGCAATTT	50
5	TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA	100
	CATTCTTTTA TTCTTGCATC GCTATAAAGA AGTA	134
10	(2) INFORMATION FOR SEQ ID :988:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 287 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :988:	
	TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGACTGTAGG ATTTGTAATT	50
	CARATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA	100
25	ATTCCTACAG AACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG	150
	GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT	200
30	TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG	250
	ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC	287
35	(2) INFORMATION FOR SEQ ID :989:	
33	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
,	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :989:	
	AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT	50
5	TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG	100
	AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCCAAC ATATTTTCTC	150
10	CTTTTCATAA AGAAGCCTAT ACACCAT	177
10	(2) INFORMATION FOR SEQ ID :990:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 158 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	•	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :990:	
	TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA	50
25	TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA	100
٠	CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC	150
20	CAAAAGTC	158
30	(2) INFORMATION FOR SEQ ID :991:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 267 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

	TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTTAAA	50
	AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT	100
5	TACACAAAAA TAAGGCAAAC TAAATGATTC AGAACAATTC AATTTAACTG	150
	AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAAG ACTTAGCGCA	· 200
10	CATAAAACAA TCACGAAGAT CACAATTTCA GCACAAATAT CTGAAGGAAT	250
10	ACACGCAAAA CATCATA	267
	(2) INFORMATION FOR SEQ ID :992:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 199 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(b) Iolobott Ilmoul	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :992:	
25	AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA	50
	TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT	100
30	CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA	150
	TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA	199
•	(2) INFORMATION FOR SEQ ID :993:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :993:	·
	TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG	50
5	ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG	100
	AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT	150
10	AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC	198
10	(2) INFORMATION FOR SEQ ID :994:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 183 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :994:	
	GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT	50
25	CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGACTGGAGA	100
	GAATAACAGA CGTGGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA	150
30	AAAAAAAAA ACAACAAACC CCAACAAACT CAA	183
30	(2) INFORMATION FOR SEQ ID :995:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	• (D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :995:

50

504

	ACCTCTGCAT TAACACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT	50
	TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTCG	100
5	GGTTACCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT	150
	TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA	199
	(2) INFORMATION FOR SEQ ID :996:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 177 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	\	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :996:	٠
20		
	GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG	50
	GTCCAATTTT CCACCTGGGG TTTAAAAGTT AAGGAGGACC AGCCTGGGAA	100
25	CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA	150
	AGGGGACACC ATATGGAGAT TTTATGC	177
30	(2) INFORMATION FOR SEQ ID :997:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 229 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :997:	
40	· · · · · · · · · · · · · · · · · · ·	

GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT

•	GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC	100
	AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC	150
5	GTAGAAAGTT GCTTGAAATT CTTTTCCTAA AAAAATTTAA TTTTTCTATC	200
	TCAAAATGAC CGTATGCAAA CGAACATTA	229
	(2) INFORMATION FOR SEQ ID :998:	
10		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 233 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID:998:	
-	TTGCAGTGTT TATGCCCGCC TTCTTTCACG GGCAGGTTCA ATTTCACTGG	50
	TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG	100
25	GTCCCTTAAT TTAAGGAACA AGTTGATTTA TGCTACCTTT TTGCACGGTT	150
	TAGGGTACCG CGGCCGTTAA ACATGTGTTC ACTGGGCCAG GCGGTGCCTC	200
30	TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT	233
	(2) INFORMATION FOR SEQ ID :999:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 216 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		

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(xi) SEQUENCE DESCRIPTION: SEQ ID :999:

	TCAAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTTGGCTT	50
	CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA	100
5	TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAAACCACC	150
	AGTGGAAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC	200
	TATCATGATA TTAGTT	. 216
10	(2) INFORMATION FOR SEQ ID :1000:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 280 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:	
	GACAAGACCT AGAAGCAACA ATGCCCAGTA GAAACAAACA CACCTACTGC	50
25	CTGGATCTTA GTTTTTAATT ATATTCCCCA ATAAAGAGAC CCAGGGCTCC	100
	TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA	150
30	CCTAGAATAT CTAATACTGC CAAAAATTAA GAAAGTGTTC TAAAAAAAAT	200
30	CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC	250
	CCAATGGCCA AAGATCAAAT AATTTTTCAA	280
35	(2) INFORMATION FOR SEQ ID :1001:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 324 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	ADA MODOLOGY. linoar	

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(xi) SEQUENCE DESCRIPTION: SEQ ID.:1001:

	·	
5	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
5	CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGGAAGCTTA	100
	GTGCTTTCAG CCCCATTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC TGTTCATTTG TATC	324
	(2) INFORMATION FOR SEQ ID :1002:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 254 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:	٠
30	ATTTCCATTC ATAAGTCCTC ACAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCTCCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCCTCC TCCAGCAAGC TTCTTAATTC	250
40		
40	ATTT	254

(2) INFORMATION FOR SEQ ID :1003:

508

(A) LENGTH: 265 base pairs

(i) SEQUENCE CHARACTERISTICS:

5	(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1003: AAGGTTGCGC TGCCCATCCT CTCGCCCTTC GGAATTTACC CCTGGCCGCT	50
	CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA	100
15	TTGCCTTTAT ATTTAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC	150
	ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG	200
20	CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTCACGTCG	250
	TTTGAGACTA TACTG	265
	(2) INFORMATION FOR SEQ ID :1004:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
30	' (D) TOPOLOGY: linear	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1004:	
35	AAATATGCCC TGAGGATTAT CTGATGTCGA TGGTGTGGAA AAGAACTCCA	50
	GCAGGCGACT TOGUATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT	100
40	AGCAGACGCT GCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC	150
	GAGCTTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTTAA	200

509

	TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG	250
	CCCCAGGTGA CCA	263
. 5	(2) INFORMATION FOR SEQ ID :1005:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 317 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1005:	
	CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG	50
20	CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC	100
	TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA	150
	GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTCGAATT	200
25	GTAAAATCGT GAGCCACTCA TATTCAAACT AAAAAAAGAA CAGAACTTTT	250
	ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA	300
30	CGCTTGCATT CATAAAG	317
	(2) INFORMATION FOR SEQ ID :1006:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 287 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

•	CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCCT GGAATGCCTT	50
	TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACCTAG	100
5	CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC	150
	TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA	200
	TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA	250
10	GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT	287
	(2) INFORMATION FOR SEQ ID :1007:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 273 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	·
20	(D) TOPOLOGY: linear	
	· · ·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:	
25	GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA	50
	CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA	100
30	TGCTGTATTC AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG	150
30	TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA	200
	ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA	250
35	TATTCGGATT TTACCGTAAG GAA	273
	(2) INFORMATION FOR SEQ ID :1008:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 308 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

511

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :1008:	
	TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT	50
10	TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC	100
10	CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT	150
	GCGCCCTCTC CCTGCCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA	200
15	TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG	250
	GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG	300
20	CAAAAAA	308
	(2) INFORMATION FOR SEQ ID :1009:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 187 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) TOPOLOGI. IIMeat	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1009:	
	GAACCGCCTC TGTTTCCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA	50
35	GCAGTTTTGA AAACTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA	100
	GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAACTAA TGAGTGTCAC	150
40	TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA	187
	(2) INFORMATION FOR SEQ ID :1010:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1010:	
10	AAGAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG	5
	ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA	10
15	AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT	15
	AAGCTACTTC TCCTTGATAT TACCT	17
	(2) INFORMATION FOR SEQ ID :1011:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 208 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1011:	
30	TGAAAATAT TTGGAACTCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA	5
	GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA	10
35	CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT	15
	ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG	20
	TATTTTAT	20
40	(2) INFORMATION FOR SEC ID .1012.	

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

513
(i) SEQUENCE CHARACTERISTICS:

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:	
	ATGATATCTA GACTACCAGT ATTTTTTGAA TGAGGCTTTC TTAGGAGTAT	50
	GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG	100
15	ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG	150
	ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA	184
20	(2) INFORMATION FOR SEQ ID :1013:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 263 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	•	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:	
	CTTTGACATT TGATCAGACC AAACAGTGCT GTTTCCCGGG GAGGAAACAC	50
	ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC	100
35	ATACCTTGTT TATCAAATGA GCGACTCAAA ATGATTAAAA ATAATGCTGT	150
	TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC	200
	CGGAAAGAAG CATTTTTGAT ACTTTACTGC GAGTCAAAAA TCAATACGCA	250
40	GAATGGCATT TGA	263

514

(2) INFORMATION FOR SEQ ID :1014:

. 5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1014:	
	CARATTARGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACGACA	50
15	TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT	100
	AAAAAAAAT ATGACCAGGA TACAAGGACA CTTCACCGTT TTTAACCCAC	150
	ACAAGGTCAG GTAATGTTTA CCTTGAAACA CAATCGCATA TGACCCTTTA	200
20	TGCCACTCAC CTAGGCCTTT AATAATGAG	229
	(2) INFORMATION FOR SEQ ID :1015:	
25 30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 246 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1015:	
35	GAAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT	50
	ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG	100
40	TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC	150

ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTCA

	TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA	246
	(2) INFORMATION FOR SEQ ID :1016:	٠
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 287 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1016:	
15	TTCATAATCG CTGGCACTGA ACAAAGTTGC AGAATTCTTT GCCAGGTACT	50
	TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC	100
	AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG	150
20	ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA	200
	GAATTTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC	250
25	AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA	287
	(2) INFORMATION FOR SEQ ID :1017:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 299 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1017:	
40	ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA	50
40	CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTTGAA ATGCTGTTTG	100

	TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG	150
	TTAACCACAA TCAGTTCTAC ATAATTTAAC AGAAAACATC TGGTGGCACT	200
5	TTTAAATGTT TAAGGACAGC ATTTCACAAA CTAAGCCCGC CCCCAGTCCC	250
	ACTGCAGCAG GAGAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA	· 299
	(2) INFORMATION FOR SEQ ID :1018:	
10	encurry of our promptication.	•
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(b) Torobodi. Timear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:	
20		
	ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT	50
	GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT	100
	•	
25	TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG	150
	TGGGTTTGAG GTGGGCCCAA GAATTTCCCT TTTTAACAAG TTCCCAGAAG	200
	ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTC	250
30		274
	AAGAGGACAA TCTAAAGTGC TCCC	2/4
	TO THE PROPERTY OF THE TOTAL TO THE TOTAL TOTAL TO THE TO	
	(2) INFORMATION FOR SEQ ID :1019:	
35	(i) SEQUENCE CHARACTERISTICS:	
33	(A) LENGTH: 232 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(-, 2-2-2	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:	
	TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA	50
5	CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
	CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
10	AAATGGCACC TCATCTTTGA TCAAAGATTC AG	232
	(2) INFORMATION FOR SEQ ID :1020:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 133 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:	
25	AACAGTCCAT GCTGATCTTA GTAACTATGA TGAAGATGGT GCTTGGCCTG	50
	TTCTTCTTGA TGAATTTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG	100
20	CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC	133
30	(2) INFORMATION FOR SEQ ID :1021:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 280 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		•
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:	

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•	TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT	ā
	ATTTAAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG	100
5	ACTGTTGAAA GTTTAAGTAT TAGTAAACTT GAGTTACTTT TTCTTTCAAA	150
	TTTCACTCCG CTTCCCTGCA TTTCGAAGCT GCTCTTTCTG GTCCTACCCA	200
••	CCACCCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG	250
10	TATTGGGGAT CCATTGTCTA TATTTAAAAC	280
	(2) INFORMATION FOR SEQ ID :1022:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 304 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:	
25	AAAATAAATA ACTTCTTAGA TTTTTGACTG AAAAGATCTG AGAATGTTCT	50
,	GCCAAACAGC CGACCAACTG GTGCAAAAGG TTAAGGCTGA CTTGACTTAG	100
30	CAACCTGCAG CACAACCAAA AACACTGATG CAGTTCAGAG CTCTTCAAAT	150
30	GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTŤA	200
	ATCCTCTAGA CAGTTTTCTT TTTGTTTTGC ATGCATCCCG TTCCATTTTC	250
35	ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTTGCT TTTTAATCGG	300
	TTTT	304
	(2) INFORMATION FOR SEQ ID :1023:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

519

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
_		
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:	
10	TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA	50
	CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
15	CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
	AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT	237
20	(2) INFORMATION FOR SEQ ID :1024:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 320 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:	
	GGCATGATTA TTAGAAACTA TTTAAGCTTT TTTCTTTGAA AAACAAGCTC	50
	CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC	100
35	TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT	150
	TTTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG	200
40	TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT	250
	TTCACTTGTT TAGTTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT	300

	TAGAGCCAAC AGGAATCTGC	320
	(2) INFORMATION FOR SEQ ID :1025:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 202 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1025:	
15	TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT	50
	TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA	100
20	ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG	150
	TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT	200
	CT	202
25	(2) INFORMATION FOR SEQ ID :1026:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleic acid	•
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1026:	
	ATTGGTAGAC AATATCATAA GAGTTTTCTG ATAAAAGATG CTTTTTAACC	50
	CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA	100
40	ADCETTANCE TETTCHES OF THE SECTION O	. 150

	TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTTCC AAAGAGAATA	200
	CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA	243
5	(2) INFORMATION FOR SEQ ID :1027:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 185 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1027:	
	TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA	50
	militadini diddinimi militadin madildina documilin	30
	GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTTGCCTT TATTTGCTGT	100
20	TAACTGTTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAAA	150
	CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA	185
25	(2) INFORMATION FOR SEQ ID :1028:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 312 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1028:	
	(,	
	GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC	50
	TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG	100
40	1001010000 000000100 0101000101 00000100	

	TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG	200
	TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC	250
5	CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT	300
	CTGTTCACAG TT	312
	(2) INFORMATION FOR SEQ ID :1029:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1029:	
20		
	ATTATTTATA AATTTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT	. 50
ι		100
	TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTTATTTC TTTTTTCCTG	100
25	AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT	150
	TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT	200
	TATACAGATG GAAAAAGA	218
30	Introduction Community	
	(2) INFORMATION FOR SEQ ID :1030:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 124 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

(xi) SEQUENCÉ DESCRIPTION: SEQ ID :1030:

50

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	TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA	50
	ACTACAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT	100
5	TTCTTAGTTC TTTGGACACA TCCG	124
	(2) INFORMATION FOR SEQ ID :1031:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 237 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:	
	(XI) SEQUENCE DESCRIPTION. DEG ID .1031.	
	TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTTCAGTC TGTAGCTTGC	50
20		
	CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTTAAGTTTG	100
	•	
	AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTTGTG TTCAACTAAG	150
25	GGATATTAGC TTACCATTTT TCTCGGTTGA ATATTATGTG TTTATAGACA	200
	AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC	237
	AGAAATGGTC ACTAMAGCAA AATAACTGAA AATTATC	237
	(2) INFORMATION FOR SEQ ID :1032:	
30	(-, -, -, -, -, -, -, -, -, -, -, -, -, -	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 147 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:	
40		

ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCCGAGT TCTAAGGCCA

	CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA	100
	GCGACTTCCT TGAAGACTGT TTTTAACATA CCAAAGGAGG ACAAGCT	147
5	(2) INFORMATION FOR SEQ ID :1033:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 238 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double.	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1033:	
	AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA	50
20	GAGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC	100
20	TTTTTACTCA TAATTCGCTT CAAGCCAACT ACGGAGGCGC ATTTACAAAA	150
,	CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA	200
25	TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTA	238
	(2) INFORMATION FOR SEQ ID :1034:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 63 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:	
40	TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT	50
40	GGACTGTGCA GGG	63

	(2) INFORMATION FOR SEQ ID :1035:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1035:	
	CGACCGGCGC TCAATGGCGA AATTCCGAGC CAGAGCTATT GGTTGAATGA	50
15	GTAGCGCTGA TGGTTTAGAT AATAACTAGT ATGGGGATAA GGGTGAGCAG	100
	GCGCCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TTAAAAGCCA	150
•	AAGCCTATAA CGGTAGCGTC TACATCACGA	180
20	(2) INFORMATION FOR SEQ ID :1036:	
•	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 142 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1036:	
	CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA	50
35	CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA	100
	CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC	142
	(2) INFORMATION FOR SEQ ID :1037:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 95 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
•		
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:	
••	CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC	50
10	TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG	95
	(2) INFORMATION FOR SEQ ID :1038:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 195 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:	
25	ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT	50
	TTGACAAAA CATACACAC TAGTACAGGT AGAACATATA ACTGGTTGAT	100
	GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT	150
30		
	CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT	195
	(2) INFORMATION FOR SEQ ID :1039:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 218 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:	
	GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAGACAT	50
5	TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTC TAAGATGAGG	100
	TTAAGTTTCT TAACAAAAGA ATAAACAACT GTGACTCTAT CTGTCGGGGG	150
	AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAA	200
10	CGAGACTTTG ATGGAGAC	218
	(2) INFORMATION FOR SEQ ID :1040:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 318 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:	
25	TTTATTATTT TGAATGATTT AATGGTTTTC TACACAATTT ACATCACAAC	50
	ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC	100
30	CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG	150
30	CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG	200
	CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA	250
35	CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTTC TCAATCCTGA	300
	AATCCCCTAG GGAAGGGG	318
40	(2) INFORMATION FOR SEQ ID :1041:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	

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(B) TYPE: nucleic acid(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:	
	ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
10	TGCCGCCGAG GCGGTGGACC GCATCACGGT GGCGCTGACG AACGCGAGAT	100
	TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
15	TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCCGCCG GTGCCGGGC	199
	(2) INFORMATION FOR SEQ ID :1042:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 300 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:	
30	GCCTCTAACA AAACTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
30	CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
	CCCAGGCAGA CTTCGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG	150
35	ATTGTCCAAA ACAAAGAAAC ATGTCAGCAG GGCCTATGGT GGTTCCATGT	200
	GTGCTAAATG TGTTCGTGAC AGGATCAAGC GTGCTTTCCT TATCGAGGAG	. 250
	CAGAAAATTC GTTGTGAAAG TGTTGAAGGC ACAAGGCACA ATGTCTGGAA	300
40	(2) INFORMATION FOR SEQ ID :1043:	

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(A) LENGTH: 170 base pairs

(i) SEQUENCE CHARACTERISTICS:

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:	
10	GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA	50
	GTCTGGGATG AAGCGGCCTC CTCCCTGTCT TGCCCTCCAA AATTGAGTCT	100
15	GGCCTGATTC CTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA	150
	CACGGTGAAA CTGGAAAACC	170
	(2) INFORMATION FOR SEQ ID :1044:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 260 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:	
	GGCCCCCCT GGGGACTGCT GGTTTCCAGG GGCCACCCCC CCTCATCCAA	5
	AAGAAGAATC AAGTTTTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT	10
35	CACCTCGAGC TTCCACTTGG GCCCTTTCCC ATGCTTCTAC TTGAGCCCCG	15
	CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT	20
	GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT	25
40	TTTTTTTT	26

	(2) INFORMATION FOR SEQ ID :1045:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 164 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
10	A CONTROL DECORTERION, SEC. ID +1045.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1045:	
	AAATCTATAA TTTTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG	50
15	TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT	100
	AAGTGATTAT CTTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG	150
20	GCACTGATGT GTTG	164
20	(2) INFORMATION FOR SEQ ID :1046:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 130 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	4	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1046:	
	TCCCTCCTTT CCGAACTGGA GCCCCATCCT CTCCAGAGTA TCCAGGGCTT	50
35	CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT	100
	ACTGTCAACC AGTCTTTGCT GCATAGGCAT	130
	(2) INFORMATION FOR SEQ ID :1047:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(1) SEQUENCE CHARACTERISTICS.	

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(B) TYPE: nucleic acid(C) STRANDEDNESS: double

		(D) TOPOLOGY: linear	
5			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:	
10		GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC	50
10		AGTGGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA	100
		CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG	150
15		TGAATCTCCA TTCGAGGAAG GGGAAGAAGA GCTCGGAGGG TGACAGCCTC	200
		CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTTCCTCCTG	250
20		ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA	285
20		(2) INFORMATION FOR SEQ ID :1048:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 233 base pairs	
25		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
		(b) Torozoor: Tracar	
30			
		(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:	
		TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA	50
35	ø	CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC	100
		CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC	150
40		GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC	200
40		CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA	233

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	(2) INFORMATION FOR SEQ ID :1049:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 293 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	TO TO 1049	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1049:	
	ACTITAATIT ATTICGGATG CCGGAATIGI GCCCAGAGII TCTCCIGAGC	50
15	TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG	100
	AACTCTGAGC TGTCCTTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC	150
	TTAATTCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT	200
20	CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTC	250
	GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCGA TAC	293
25	(2) INFORMATION FOR SEQ ID :1050:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 219 base pairs	
30	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	· .
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1050:	
	AAAACTATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA	50
	COLORS AMON AMONAMA CARO ARMONAMA AMONAMACO COR CAMAAAMACO	100

AGATCAAAAG TCCTGTTTCA GTAATTTGAT TAAACTGTAG AATACTAAAA

	AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC	200
	AGTATATACC TAATGGCTA	219
5	(2) INFORMATION FOR SEQ ID :1051:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 70 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1051:	
	AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTTTGAT TTTTCGTTTT	50
	TGCGATAGTT TACTGAGAAC	. 70
20		
	(2) INFORMATION FOR SEQ ID :1052:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 204 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1052:	
	ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC	50
35	CTGCCGATGA TTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC	100
	CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTTTA	150
40	TCTCAAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG	200
40	ጥአጥጥ	204

150

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	(2) INFORMATION FOR SEQ ID :1053:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 252 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1053:	
	ACTANACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT	50
15	AAGAGAGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG	100
	AGGTATAAAA GGTATCCAAG AAAAGTAAAA CATACAAAGG CAATTCAAAT	1,50
••	CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC	200
20	CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA	250
	CG	252
25	(2) INFORMATION FOR SEQ ID :1054:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs	
•	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1054:	,
-	AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA	50
	CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT	100

TTAGAGGTGT TTAGTATTTC ACTCCGTTCT GATGGAAGCA CTTTGAATGC

	TTGCATGGAG ACATAAAACT GAATATTTAA TTGACAATAG ATCATGCGCC	200
	TGTATTTATA AA	212
5	(2) INFORMATION FOR SEQ ID :1055:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 152 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1055:	
	ATAAACTGTG CTAACTAAAG TTTTTATTTC ATCAATATAA AAGCTGTAAA	50
•	AAAACTGAGG AGAAAGCAGT TGCCAAAAAG ATGAAAGAAA AACAACATAG	100
20	AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAAGT AACTCATCTC	150
	AC	152
25	(2) INFORMATION FOR SEQ ID :1056:	,
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 205 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1056:	
33	(VI) OREOWICH PURCHITITIONS DAY IN SECOND	
	AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGTT	50
40	GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG	100
40	AGATGTTGTA GTCGGAGCCT CATTCCTTCC GGGGCACTGT TTCTTCTAAT	150

	GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG	200
	GCAAA	205
5	(2) INFORMATION FOR SEQ ID :1057:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 174 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1057:	
	GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC	50
	CCTTTGTCTG TTTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT	100
20	GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT	150
	GATAGCAGGT TTTAAAATGA ATCC	174
25	(2) INFORMATION FOR SEQ ID :1058:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 125 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1058:	
	TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA	50
	GCTTTAAAAT ACCATGTTGA CAGCATTTTG AATTGTTTCA TAGACGTACT	100
40	TATTTAACTG ATGCGAACAT TCACA	125

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	(2) INFORMATION FOR BEG ID .1003.	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 205 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1059:	
	TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT	50
15	TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC	100
	GTTGAAAACT TAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTTCATTATG	150
20	ACTATAAAGA AAAAAGGTTC ATCAATTCAA AAAAAAATCC TGATTCTTCA	200
20	AAATA	205
	(2) INFORMATION FOR SEQ ID :1060:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 249 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1060:	
35	ATCTCACAGA TTCTTTTCA CAGATTCATT CATGTTGAGT GAAAGAAGCC	50
	AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTTG	100
40	AAAACTAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG	150

GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT

•	ACTTGGATTT TGGGTCTA1 GCTGGCAGG GGAAGGGATA CATTGCAAA	249
	(2) INFORMATION FOR SEQ ID :1061:	
5	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 200 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:	
15	TAGCACATTG CATCCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA	50
	ARATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT	100
20	GCAGAATCAG TGGTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC	150
	TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC	200
	(2) INFORMATION FOR SEQ ID :1062:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 200 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:	
35	GCGCACAGCT GAGAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG	50
	GATGCCCATC TAAAAGTTAA GTGTCATTTC TTTTTAGATG TTTTACCTTT	100
40	ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG	150
40	ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT	200

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(2) INFORMATION FOR SEQ ID :1063:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 246 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1063:	
	TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA	50
15	ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT	100
	GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT	150
20	TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC	200
	AAATTCAAAT CTCAAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA	246
	(2) INFORMATION FOR SEQ ID :1064:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 170 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1064:	
35	CCCTCATGTG CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC	50
	AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT	100
40	TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA	150
40	TOCACOCTOS ACTOACCOAC	170

	(2) INFORMATION FO' SEQ ID :1065:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 171 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1065:	
	CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTTCATT	50
15	GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG	100
	AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC	150
20	AAAAGAGAGG AAGATGGGGT G	171
20	(2) INFORMATION FOR SEQ ID :1066:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 201 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1066:	
	GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT	50
35	ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC	100
	TCATACACAG CTTCATGGGT TTACTTTCCC AAGCACTTCC TCCCTCCCTG	150
40	CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTCC CCTTTTTCAA	200
40		201

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	(2) INFORMATION FOR SEQ ID :1067:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 151 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1067:	
	ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT	5
15	GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG	100
	GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG	150
20	c	15:
	(2) INFORMATION FOR SEQ ID :1068:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 273 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1068:	
	ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG	50
35	ATCTGTTTGC TCCTTTGAGT CTCCCTTTTA CTTTACAACT AGAAAACCAA	100
	TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC	150
	することにでするる みですすることがな みでみででででして とてするととですする とにすととですでする	200

AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTTGGAA

250

	ACTGACTTTA AAGAAAACAT ACA	27:
	(2) INFORMATION FOR SEQ ID :1069:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 189 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
10		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:	
15	CAATCTTGCT TATAAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT	50
	TCCTGGTGCA ATTGTGATTT TTTTTTAGCC AAAATGAATG GCAAACTCTA	100
20	TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACTCTT AATCAACGTT	150
	TATTACACTT TTATAAAGGC AAACTACGCG AAAGAGCCC	189
	(2) INFORMATION FOR SEQ ID :1070:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 280 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
30	(D) TOPOLOGI: Tinear	·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:	
35	TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT	50
,	TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG	100
40	TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC	150
	ATGARTCACG ACTTCTCATC CCGTTTTATC AGAGTGCATA TACGTCCTAC	200

	TTAAGGAAÄA GTAAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT	250
	AAGCATTTTA ATAAAAAGTC AGAAGGAATT	280
5	(2) INFORMATION FOR SEQ ID :1071:	
	(i) SEQUENCE CHARACTERISTICS:	. •
	(A) LENGTH: 193 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1071:	
•	AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC	50
	TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA	100
20	GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA	150
	GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG	193
25	(2) INFORMATION FOR SEQ ID :1072:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 175 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1072:	
	AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCCAGATA GGCCACGCGC	50
40	AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC	100
40	CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG	150

	TCAAGTTCCC CTCGAGATTC ACATC	175
	(2) INFORMATION FOR SEQ ID :1073:	٠
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 339 base pairs	
	(B) TYPE: nucleic acid	٠
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUE CE DESCRIPTION: SEQ ID :1073:	
15	AGTGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG	50
	GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG	100
20	GTGGACAGGC TAATTTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTTCA	150
	AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT	200
	TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA	250
25	TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA	300
	TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA	339
30	(2) INFORMATION FOR SEQ ID :1074:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 172 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(D) IOFOLOGI. IIMEAI	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:	
40	ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCAGT TTGAATCTTC	50

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	CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA	100
	ATCAAGAAAC TCGGACCCAA CTTGGTGCAA AGACGGATCT CCGCCGATTC	150
. 5	TGACGGCTCT CCAGGTTTTG TC	172
	(2) INFORMATION FOR SEQ ID :1075:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 299 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPÓLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1075:	
20	AGAGTAGGAA GAGGGAGGG AACAGGCATC TAAGATAGAC TTTCTCCATC	50
20	TGTTGGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTTCAT ACACTTCAGT	100
	CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG	150
25	CCTGCAAATG AGACCACTCT CATTTCTCAG TTTCGATTTG ATTCACTCAC	200
	TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG	250
30	GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTACTGATG	299
30	(2) INFORMATION FOR SEQ ID :1076:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 283 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
•		

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(xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

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	GCCCTCATCG GCGATACTGG AGGTTCGCTT TCTCAACCCT GTGGGCTTCA	50
	CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC	100
5	ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG	150
	AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG	200
	CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA	250
10	TCATTCGAAG TATTGCTATG AGCAGTGCGA AAA	283
	(2) INFORMATION FOR SEQ ID :1077:	
15	(i) SEOUENCE CHARACTERISTICS:	
	(A) LENGTH: 297 base pairs	
	(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:	
25	ACCAATCAAG TACACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC	50
	AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAAACTC GAATAAGAAG	100
30	TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA	150
30	GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA	200
	GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTTCAGGC TGGAAAACTA	250
35	TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC	297
	(2) INFORMATION FOR SEQ ID :1078:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 291 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :1078:	
	AATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC	50
	AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA	100
10	GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG	150
	TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTCAGA TAATCATAAC	200
15	ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA	250
	GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G	291
20	(2) INFORMATION FOR SEQ ID :1079:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 136 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	·
	•	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1079:	
	AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG	50
	CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA	100
35	AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA	136
	(2) INFORMATION FOR SEQ ID :1080:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 300 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS, double	

548

(D) TOPOLOGY: linear

	·	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID :1080:	
	CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT	50
	GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA	100
10	GCTGCGGTAT TAAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG	150
	AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT	200
15	CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA	250
	CACATTGGAG TCACGCGGCC TGCGTAAGAG TATGAAGGTC TTCCTGTAAA	300
	(2) INFORMATION FOR SEQ ID :1081:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 219 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	A IN CROUDING PROCEDING ON CRO ID 410914	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1081:	
30	GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA	50
	AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT	100
35	ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC	150
	TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA	200
	CTGAAGGTGC TGGACATGA	219
40	(2) INFORMATION FOR SEQ ID :1082:	

> 549 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1082:	
10	ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG	50
	AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG	100
15	CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT	150
	GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC	200
20	CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA	250
	GTCTCAGCTA GAGGGAGCGT GTCATTTCTG CCTTAGTGGT TTGCCTGCGA	300
	CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACTT	350
25	GTCGGAAGTT	360
	(2) INFORMATION FOR SEQ ID :1083:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 250 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1083:	
40	CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT	50
	CTTTCAATTA AATACACTCC AAGACATCGA GTTTGGCAGA TATTGCGCCC	100

	GCCGTTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT	150
	AGACATTTGC TTGAAATTTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT	200
5	GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAA AAAGTTCCAG	250
	(2) INFORMATION FOR SEQ ID :1084:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 261 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1084:	
	TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTC TTGTCTAGTG	50
20	TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTTG GGGAGAGTGA	100
·	AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG	150
25	GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTAAA	200
	AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAA AATTTNTTAA	250
	GTTTTAATAG G	261
30	(2) INFORMATION FOR SEQ ID :1085:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 260 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
-		

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(xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

	GCAATCCATA AGTGTCCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT	50
•	CTTCATGATC TTTTTCGATT TTAAAATGTC ATGCAATTTT AGAGAAAAGC	100
5	TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA	150
	TCACTTTTC ACTTTCCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC	200
	TTANTACACC AGÁCAAGAAC ACACTATGAA TGCGAGACAG AGGGAGACAG	250
10	AGGCGAAATA	260
	(2) INFORMATION FOR SEQ ID :1086:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 213 base pairs(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:	
25	AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT	50
	TCGGAAGCTA TGGATTTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA	100
	TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA	150
30	CGAATTTCCT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTTAAGGGAA	200
	GACAAGACGG ACT	213
35	(2) INFORMATION FOR SEQ ID :1087:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 256 base pairs(B) TYPE: nucleic acid	
40	<pre>(C) STRANDEDNESS: double (D) TOPOLOGY: linear</pre>	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :1087:	
	TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG	5(
5	TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTTGAAA	10
	TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG	150
10	ATCATTTCTC AGTCCTATTT CTCAGTTCTA TTATTTGAGA ACCTAGTCAG	200
	TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT	250
15	TTTTTT	25
13	(2) INFORMATION FOR SEQ ID :1088:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID :1088: 	
	TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC	50
30	TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG	100
	GCTCTGACAG TGACAGGTTC TTCCCTCTGA AAAAAGAATA GAAGAGGAGC	150
35	TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA	200
33	AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA	250
	CTGAGGCGAG AGGC	264

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID :1089:

553

(A) LENGTH: 157 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1089: 10 GACCTGGAAT TTGTTTTCGT CTGTTCAGTA GACTCCGATT TCAGAATATG 50 TCGGAATTTC AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG 100 TTTACATACC GAGCTGTTAG CCCCAGTCAC TGGGTCCGAA ATTACGCCGA 150 15 TACCGAC 157 (2) INFORMATION FOR SEQ ID :1090: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1090: 30 GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA 50 CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT 100 AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAACT CGATGAGAGA 150 35 GAAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT 200 CAAGTAATGG AAACTTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT 250 CCAGCAAGAT GAGAGATTTC TCTATTTTGT AACGAGTAGT CCACCGATCG 40 300 TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA 350

•	AAAAAACATA GATGTT	366
	(2) INFORMATION FOR SEQ ID :1091:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 305 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(2) 222222	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:	
15	GGTCTGAATC ATGAAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC	50
	AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTCA	100
	CACCATATGA AGACATCAAA AAACACTTAA GGATTCGAGA AAGAGAACAT	150
20	CTTTTGTTAA AGAAGAGAT AAGATTTTGG AAGAAAAGT AATAGCAAAT	200
	TTGAAGAAGA AACAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA	250
25	TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTTG AAGAGCAAAT	300
	GGACA	305
30	(2) INFORMATION FOR SEQ ID :1092:	
•	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 237 base pairs(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:	
40	AAATGGAAGT TGAACTGAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC	50

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	TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT	100
	GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG	150
5	CTTCTTTATT TTTATTATTA TTATTTTTCT TTTTGTGGAG AACAGCGTCT	200
	TGCTGTATTG CCCAGCCTGA TCTCAAACTC CTGGGCG	237
10	(2) INFORMATION FOR SEQ ID :1093:	
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 420 base pairs(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:	
20	AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGGAAGTGCA ATATCAAGGT	50
	GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA	100
25	GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA	150
	CAGTCTTCTC CATGTGTATC CTTCCTTCAG TTTCCCTTAT AGGACACCAG	200
30	TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTTGA AGTTACTCAC	250
	CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTAA GGAACTAGGA	300
	CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA	350
35	AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATACACACA TTAAGGTTTG	400
	TGGGATTCAG AAAGGTATAC	420
40	(2) INFORMATION FOR SEQ ID :1094:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5	·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:	
10	GTTTCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
10	CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG	100
	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
15	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192
	(2) INFORMATION FOR SEQ ID :1095:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 228 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:	
30	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
30	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCCC	100
	ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT	150
35	GCCAAACCAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTTCT	200
•	GCTTCTTGGA TACCTCCTTC AGGAAATC	228
40	(2) INFORMATION FOR SEQ ID :1096:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 198 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:	
	ATTTTTTATG GAAAAAGGGG GATAATGCAA AATAGCAAAA ATTGTAAACA	50
10		
	AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTAAAACACC	100
	TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTTCATTCAC	150
15	NOTICE TO A COORTINE A NORCE OF CHARGO AND A CORD OF	100
15	ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT	198
	(2) INFORMATION FOR SEQ ID :1097:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 118 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(vi) SEQUENCE DESCRIPTION, SEC ID .1007.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:	
	TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG	50
30		
	CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTTTCTAC AAAACTGTGA	100
	CACTTCAGTC AGTTTTTC	118
35	(2) INFORMATION FOR SEQ ID :1098:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 138 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
• •	(D) TOPOLOGY: linear	
	(b) Iolobot. Illeat	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:	
	AAAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT	50
5	CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG	100
	TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCNAAGG	138
10	(2) INFORMATION FOR SEQ ID :1099:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 151 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1099:	
	ACTCCACCAC TGGGNCCGCC ATGTTTTGGG TNGGNGCAAT GCGCTGTCTG	50
25	TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT ACACTGACTG	100
	ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG	150
	G	151
30	(2) INFORMATION FOR SEQ ID :1100:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 201 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :1100:	
	TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT	50

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•	CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA	100
	TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT	150
5	CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG	200
	c	201
••	(2) INFORMATION FOR SEQ ID :1101:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 212 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:	
20	TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT	50
	CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC	100
25	ATTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG	150
	TATCACTGGA GGACTGGGNC CAGGACCTGA CCTGGTGGTA CCAAAATCCA	200
30	TGAGGCNGNA AT	212
	(2) INFORMATION FOR SEQ ID :1102:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 218 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40		
40		

(xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

•	CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG	50
	GTTCGTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT	100
5	GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC	150
	AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN	200
10	GAGTGGAAAT TCCANCAT	218
10	(2) INFORMATION FOR SEQ ID :1103:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 207 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:	
	GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT	50
25	TCGTGTAAGT ACACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG	100
	CATTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA	150
30	GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC	200
	ATGAGCĢ	207
	(2) INFORMATION FOR SEQ ID :1104:	
35	(i) SEQUENCE CHARACTERISTICS:	
·	(A) LENGTH: 259 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:	
	GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG	50
5	ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC	100
	TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCTGAAC	150
10	AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT	200
	CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN	250
	GTGNAGGCC	259
15	(2) INFORMATION FOR SEQ ID :1105:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 230 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :1105:	
	ACATGACCCC TTGGACTGAA GGCGCTCAGT AGTAAAGGAG TGTCATGCAG	50
30	GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA	100
30	CGGGGACTTC TGGGAGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG	150
	CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC	200
35	ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT	230
	(2) INFORMATION FOR SEQ ID :1106:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 163 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :1106:	
٠	ACATGNOCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT	50
	CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA	100
10	GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG	150
	GTNAGAGGGG GCT	163
15	(2) INFORMATION FOR SEQ ID :1107:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 182 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	,
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :1107:	
	ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA	50
	GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT	100
30	GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA	150
	GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT	182
35	(2) INFORMATION FOR SEQ ID :1108:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 214 base pairs	
•	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1108:	
	CCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTCATGC AGGTCAACAC	50
5	ATGTCGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT	100
	TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG	150
10	AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT	200
	CGNGCCTTGA AAGA	214
15	(2) INFORMATION FOR SEQ ID :1109:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 133 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(4) 20000000	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:	
25	•	
	ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCATGCAG	50
	GTCAACACC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC	100
30	ACAGGACTTT TGGGGGGGT GGACAGGTAT TAT	133
	· · · · · · · · · · · · · · · · · · ·	
	(2) INFORMATION FOR SEQ ID :1110:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 156 base pairs	
33	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(5) 1110011 111001	
40		
	•	

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(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

	GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTCATG	50
	CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA	100
5	TGCACGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT	150
	GGAATG	156
	(2) INFORMATION FOR SEQ ID :1111:	
10		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 282 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1111:	
20	(XI) SEQUENCE DESCRIPTION. DBQ ID 11111.	
20	GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCGC	50
	AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC	100
25	ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA	150
	AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT	200
	CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT	250
30		
	GCATACACCA CGAAATACTA CGAGCCATAA AA	282
	(2) INFORMATION FOR SEQ ID :1112:	
3.5	(:) CROUPINGE CUNDACTEDISTICS.	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 181 base pairs	
	(A) LENGIH: 101 base parts (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(5), 101020011 2.11041	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:	
	TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA	50
5	ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT	100
	CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATACACNAT NGTCCATCGG	150
10	AGCCCGTATN CACGCAGCTT GTCATAACTA T	181
10	(2) INFORMATION FOR SEQ ID :1113:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 278 base pairs(B) TYPE: nucleic acid	
•	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1113:	
	ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG	50
25	AACTTAAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA	100
	TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT	. 150
30	AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA	200
30	CACTCATGAA TGCGGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA	250
	AATACTACGA GCCATAAAAG GCGAAATC	278
35	(2) INFORMATION FOR SEQ ID :1114:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs	
40	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:	
٠	ACCTGCAAAC TTTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG	50
5	TGAGCCATAC AGTTTTTGTT GCAACTAGTC AACTCTCAAC TNACGTGGAC	100
	AGCATGTAAA GAACGAGAGT GACTG	125
10	(2) INFORMATION FOR SEQ ID :1115:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 157 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1115:	
	GTAGCGACCG GCGCTCATGG AATTCCGGGA CCTGCAAACT TTTTTGAAAG	50
· •	ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTTGTGCAA	100
25	CTAGTCAACT CTCAACTCAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG	150
	CTGCCGG	157
30	(2) INFORMATION FOR SEQ ID :1116:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 123 base pairs	
	(B) TYPE: nucleic acid	
. 35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID :1116:	•
	•	

CCTGCAAACT TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT

	GAGCCATACA GTTTTTGTTG CAACTAGTCA ACTCTCAACT NACGTGGACA	100
	GCATGTAAAG AACGAGAGTG ACT	123
5	(2) INFORMATION FOR SEQ ID :1117:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 125 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1117:	
	ACCTGCAAAC TTTTTTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG	50
20	TGAGCCATAC AGTTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC	100
20	AGCATGTAAA TGGATGGGAG TGGCT	125
	(2) INFORMATION FOR SEQ ID :1118:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 125 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:	
35	ACCTGCAAAC TTTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTTT	50
	GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTTCACCGTG	100
40	GACAGCATGT AAATGGATGG GAGTG	125
40	(2) INFORMATION FOR SEQ ID :1119:	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs(B) TYPE: nucleic acid

•	(C) STRANDEDNESS: double	
, 5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1119:	
10	ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT	50
	CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT	100
15 ⁻	CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA	148
	(2) INFORMATION FOR SEQ ID :1120:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 240 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1120:	
30	AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT	50
30	AATCAAGAAA AAATAGCACC AACAACAATG AGGAGAAAAT GGAAAAAGGG	100
	CAGAGTATTT CALCGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT	150
35	TAAGCCTTCA GTTTGCCCTG TAAGCAAACT GAAGACGTGC AAGTCATCCT	200
	TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAA: 72.3	240
	(2) INFORMATION FOR SEQ ID :1121:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 254 base pairs	

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: doubl

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:	
10	AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG	50
10	GTGAGACTAA TAAGAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA	100
	AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG	150
15	ATTTTTAAGC CTTCACGTCT GCCCTGTAAG CAAACTGAAG ACGTGCAAGT	200
	CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG	250
20	ACAG	254
20	(2) INFORMATION FOR SEQ ID :1122:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 253 base pairs (B) TYPE: nucleic acid	
23	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:	
	AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC	50
35	NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA	100
	TGGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA	150
40 .	ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG	200
70		

TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC

	GAG	253
	(2) INFORMATION FOR SEQ ID :1123:	·
5 .	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 210 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:	
15	AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT	50
	GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAATCCGA GAAAATGGAA	100
20	AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT	150
	GATTTTTAAG CCTTCACGTC TGCCCTGTAA GCAAACTGAA GACGTGCAAG	200
	TCATCCTTTG	210
25	(2) INFORMATION FOR SEQ ID :1124:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 231 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1124:	
	AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC	50
40.	CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA	100
	TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC	150

	AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC	200
	GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T	231
5		
	(2) INFORMATION FOR SEQ ID :1125:	. •
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 89 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:	
	AAGTCCCATC AGCAACCCGT TTTTTACCAG ATGTCACTCA AGAATGCGCC	50
20	CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT	89
	(2) INFORMATION FOR SEQ ID :1126:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 205 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:	
25	AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA	50
35	ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC	100
-	ACCARTACTG ACARTTGTAG CGGTARTACA TACARTGATT TARTARGCCT	150
40	ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTTAGGC	200
	СТАСТ	205

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(2) INFORMATION FOR SEQ ID :1127:

5 ·	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 151 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1127:	
	GCAAGGCCTG GCCGACAACA CCCTTATTGC TAAAGTAAAT AATGNCGCGC	50
15	GGGGCCTGGA CCACCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG	100
	TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA	150
20	A	151
20	(2) INFORMATION FOR SEQ ID :1128:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 237 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1128:	
	GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCCTACCC CCCTCAGCAA	50
35	GCCGGAGAGG CTAGCCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC	100
•	CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT	150
40	GACAGACGAG ACCTGCCAGG ACGCAGCCAT TGCGGGCTGC AAGGCCTCRC	200
70	CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT	237

	(2) INFORMATION FOR SEQ ID :1129:	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 126 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1129:	
	GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG	50
15	CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT	100
	CCTTAAGATC ATCCAACTAT AGGATG	126
	(2) INFORMATION FOR SEQ ID :1130:	
20	. (i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 246 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	,
	·	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1130:	
30	GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG	50
	AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT	100
35	CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG	150
	TTTATTTGCA AGGATTTTTC TTTCGRGGGC GGAGGGGAGA GAAAAGTAAA	200
40	TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC	246
40	(2) INFORMATION FOR SEO ID :1131:	•

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs(B) TYPE: nucl ic acid

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
		·
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1131:	
10	CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA	5
	CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA	3
	TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT	10
15	TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT	. 15
15	TITCACCETC AMAGIATANA MAGIATGANA NATANACANG CICTIGCACT	15
	GTACACTTAG AAGTGTACAA TTAAAGCATT ATAGAGCTAT CTACACACCG	200
	ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG	25
20	ATAMICCON ICONATCITO NATAATCCAT CANTACGIAG AACGCAAGGG	25
	TGCAGACAGA ACTAAAACCA ACT	27
	(2) INFORMATION FOR SEQ ID :1132:	
	(2) INFORMATION FOR SEQ ID .1132.	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 329 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1132:	
35	GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG	50
	TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC	100
40	CTTAGACATT CTTCCAGGCA GGATCAAACT CAAAGGAAAA GGAATTTGTG	150
••	AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG	200

	AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA	250
	AGCCAATGTA TCTGACCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT	300
5	ATTTCTGTTT GTTAAAAAGT TCAGAATTT	329
	(2) INFORMATION FOR SEQ ID :1133:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 24 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:	
	CCCCGAGCTA GTTGTCCCGA CCTG	24
20	(2) INFORMATION FOR SEQ ID :1134:	
•	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 297 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) ToroLogi: Timear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:	
	GAGGATCCAC AAACCATGGA ACACTCTCGC GGCTGCCACT CCCCCATGAC	50
35	CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA	100
٠	TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG	150
40	CGGCCCTGC CGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT	200
70	CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA	250

	CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY	297
	(2) INFORMATION FOR SEQ ID :1135:	
. 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 93 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:	
15	GCCGCTTTAC TGCTCAGTTC GGAGCTACCG CTTCGAAAGC AACAAAAAAG	50
	CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA	93
20	(2) INFORMATION FOR SEQ ID :1136:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 334 base pairs	
٠	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	•	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:	
30	CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG	50
	TTGTGGGAGA TAACGGTGGC ATAGTTCCCT GATGCCCGGG CCAGCTTGCC	100
35	ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA	150
	TGGTGCCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG	200
•		
	CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC	250
40	0000000000	

	GCCCTCRAA CCCGGGGCTA TACACGTCAA AATC	334
	(2) INFORMATION FOR SEQ ID :1137:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 199 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:	
15	CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG	50
	ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY	100
20	AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT	150
20	CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT	199
	(2) INFORMATION FOR SEQ ID :1138:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 304 base pairs	•
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:	
35	CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCGCGT	50
	GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG	100
40	TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC	150
40	ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG	200

	TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT	250
	TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG	300
5	AAGG	304
	(2) INFORMATION FOR SEQ ID :1139:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 277 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:	٠
	GAGGATCCGG GTACCATGAG AAACTTTGAA GCCAGAGATT TTAAACAATC	50
20	AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA	100
	CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC	150
25	CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA	200
•	GTTTGTCATT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC	250
30	CACTACTGGC TAAAGAAACT AAGTAAA	277
	(2) INFORMATION FOR SEQ ID :1140:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 208 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
~ .	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

•	CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA	50
	AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT	100
5	TTTAGCAGAG CAAATTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG	150
	GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTTCA GACTGGGCTC	200
	CAGCTTCT	208
10	(2) INFORMATION FOR SEQ ID :1141:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 274 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:	
	CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG	50
	CONGGRICCO AGTACCATOG CCTCGAACTG AGCATCAATA TATTCTACTG	50
25	CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG	100
	TCAACAATGG TTAACTTCAG CCGTACATTG CTTTCCTGAA GCTCATAACT	150
	TORROWNTOO TEMOSTOR CONTROLLED CITTOOTOM GOTCATAGET	130
30	TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT	200
30	TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT	250
	GTCTCACCAA TACAAAGGAT GTTG	274
35	(2) INFORMATION FOR SEQ ID :1142:	
	· · · · · · · · · · · · · · · · · · ·	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 226 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1142:	
	GCCTGCACAT TGACTGTGGG AAACTCGGAA ACAAGCTCAC ATCTCCCCGT	50
5 _.	GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAACTG CAGTTGCCAC	100
	CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTGC ATTCCCTTCA	150
10	TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG	200
	TTAGTGTCCT ATGGTAACAC CTTCTT	226
15	(2) INFORMATION FOR SEQ ID :1143:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 168 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:	
23	RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC	50
	TGRCRCGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN	100
30	TAGGTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG	150
	GNANGRTGNN GTGGAGRG	168
35	(2) INFORMATION FOR SEQ ID :1144:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:	
	CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT	50
5	TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC	100
	CAGGATTTGA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT	150
10	CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT	200
10	AAACAACCTT ATAGTGTTTT CGCTTTGAAT TGTATGAATT CTTAGAACTG	250
	AGAAGT	256
15	(2) INFORMATION FOR SEQ ID :1145:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 184 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID :1145:	
	AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA	50
30	GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG	100
30	TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT	150
-	GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG	184
35	(2) INFORMATION FOR SEQ ID :1146:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 221 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:	
	CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG	50
5	CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG	100
	ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT	150
10	TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG	200
	GTGCTGAGAA GAATGCACAA G	221
15	(2) INFORMATION FOR SEQ ID :1147:	
13	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 255 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(5) 10100011 1211011	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1147:	
25	CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT	50
	TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT	100
30	TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC	150
	CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC	200
35	RRTMATTCTT AACANCAAAC NGMGMCTGNN NTCCCRNCTT ATAACCMAAA	250
	GATNT	255
	(2) INFORMATION FOR SEQ ID :1148:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 230 base pairs	
	(B) TYPE: nucleic acid	

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583

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:	
	(XI) DESCRIPTION. DESCRIPTION.	
	CGAGGATCCA GGTACCATGG ACGATTCACA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTCACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC	150
15	CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
13	AGTCGGTGAC GCCCGATTTG GATCGGGTGT	230
	(2) INFORMATION FOR SEQ ID :1149:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 223 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:	
30	GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTTGAGACG TTCTCCTTTC	100
35	AGGCAGAAAT CGCCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
	AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAATT CGATATAAAA GCT	223
40	(2) INFORMATION FOR SEQ ID :1150:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:	
10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	5(
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGATC CTAATGCCCT	10
	ATGATCACGT GGAACTAACA T CAATGACA TGAAGAACGT GCCAGAAGCC	15
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	20
	CTTTATGTCC AAGAACAAGG ATGCGATGGG TATTTCGTGA NGCTATTTGA	25
20	NMTRAGGRMA GNCTGNAAGG TM	27
	(2) INFORMATION FOR SEQ ID :1151:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:	
	TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA	5
35	AAAAAAACCT GAAAAAGAAA AAAAACAAAA AAGCTCAAAA GCAATCACAA	10
	GGATAGTTGA ATCCCTCTTT AAACCCCCAA AGCAACCCCC	14
40	(2) INFORMATION FOR SEQ ID :1152:	,
	(i) SEQUENCE CHARACTERISTICS:	

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(A) LENGTH: 208 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID :1152: AAGGATCCGG GTACCATGTA TTCCCCCGGT ATCAGCAGAG GCGTGTACGG 10 50 GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG 100 GTCACCAAGG TAGATTTCCA GCAGCCTAGT CCAGCTGAAC GCTTTCCAGC 150 15 CTTGCTTTTT AGCAGCTTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC 200 TTTCATTG 208 20 (2) INFORMATION FOR SEQ ID :1153: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid 25 (C) STRANDEDNESS: double (D) TOPOLOGY: linear 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1153: CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCTGGA 50 TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG 100 35 CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG 150 GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG 200 40 GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA 250 GAMGCCNMAC AGGGCTRGGG ACTG 274

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	(2) INFORMATION FOR SEQ ID :1154:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 267 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	•
	•	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1154:	
	GAGGATCCAC CGACCATGGA ACACTCTCAA TGGCTGCAAC CACCCCGTGG	50
15	CCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA	100
-	CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC	150
20	CGCAGCCGCC CCTGCGAACC CTCCAACTCG TTCACACGCG CCGAAAGCCT	200
	ATTCCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG	250
	AATCCGAACT CCGCTCC	267
25	(2) INFORMATION FOR SEQ ID :1155:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 231 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	and the second s	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1155:	
	CTCAAACCCC GNTTCCCCCC TAATAAGAGC AACTAAAAAA CTTCTGATAA	50
40	CCACAATAAA AGCGTGCATT TGAGCACAAT TCAAAAGCCA ACCCCTTCGA	100

AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG

	CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC	200
	CGTCTANCAA GGCAACGGCC GCCTTTGAAT T	231
5	(2) INFORMATION FOR SEQ ID :1156:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 128 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1156:	
	GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCCA TCCACACCTG	50
20	CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG	100
	GCTCYAACMT GTGCAAGGCC GCCTTCAA	128
	(2) INFORMATION FOR SEQ ID :1157:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 126 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:	
35	GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCCGGCTCT	50
	GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCCACA AGGGCAGAAA	100
40	GGTGAGCCTT ATGCACTGCC TAAAGA	126
	(2) INFORMATION FOR SEQ ID :1158:	

	(I) SEQUENCE CHARACIERISTICS.	
	(A) LENGTH: 101 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	() CECUENCE DESCRIPTION. CEO ID .1150.	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:	
20	AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA	50
	CCCCAHACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT	100
15	T .	101
	(2) INFORMATION FOR SEQ ID :1159:	
	· · · · · · · · · · · · · · · · · · ·	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 172 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
-		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:	
		•
	GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG	50
30		
	GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC	100
	CCCACACAC GTGGCGGTGC GGGTGAACTG GAAGGGGAGG TCGAAGGTGC	150
35	CATCTTCTTC AGGCCCCTCC AC	172
	(2) INFORMATION FOR SEQ ID :1160:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 235 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

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(D) TOPOLOGY: linear

5 .	(xi) SEQUENCE DESCRIPTION: SEQ ID :1160:	
	GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA	50
10	TGGTTATTTC CCAGGACCAC ACGATTTGCC TACGTCACTG GAAGGCTATG	100
10	TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG	150
	CTTTGACCCT GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT	200
15	TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT	235
	(2) INFORMATION FOR SEQ ID :1161:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 284 base pairs	i
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	·	
	(D) TOPOLOGY: linear	
25		
23		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:	
30	GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG	50
	TTAGATACAA ATGCAAAACG CTTCCTAAAA AACGGCCTGA AAAAAAACTC	100
	ACAGACAATG CCAAACTTTA TAGGTCTGTA TTTTCCTTTA TACAAAATGC	150
35	CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG	200
·	ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA	250
40	ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA	284
	(2) INFORMATION FOR SEQ ID :1162:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

5	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:	
10	GCTCACATAA ATTTCTTCAC CGACCCTTTT CCTTCCAGCT TCCTTACTAT	50
	AAAAAACCCC ACA AATA TGTTCATCAT CATCCATACT AACCAACCCC	10
15	GTCACCATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG	150
	TTACCACCTC TAGGGGCAGA CCCCTTTTCA GATATATTCA AGAGTTTAAT	200
. 20	ATCCTCCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA	250
20	ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC	28
	(2) INFORMATION FOR SEQ ID :1163:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 122 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:	
35	GAGGATCCAA AAACCATAAA ATTCATCATC CCCAGCAGGT GCNCTAGCTA	56
	TACTITATIA CAGCAAARCA CAACCACAC CIGAMCIANM ICGIATAGAI	100
40	AAACACCAAT CATGGGTCGG CC	12:
40	(2) INFORMATION FOR SEQ ID :1164:	

(A) LENGTH: 142 base pairs

(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

	(C) STRANDEDNESS: double	
5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1164:	
10		
	GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG	50
	GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC	100
15	CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT	142
	(2) INFORMATION FOR SEQ ID :1165:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 219 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
3.5		
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1165:	
	TATTCCCCCG GTATCAGCAG AGGCGTGTAC GGGCACTGCT TTAAAACTGG	50
30		
	GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC	100
	CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT	150
		130
35	TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG	200
•	GATGAGAATA GAGAACTCA	219
	(2) INFORMATION FOR SEQ ID :1166:	
4Ó		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 202 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:	
10	GAGGATCCAC CAACCATAGA AAGGAAACAA CACTTGGAGT GAACCCGACC	50
10	CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA	100
	AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTTNT CAATCCAAAC	150
15	ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC	200
	AA	202
20	(2) INFORMATION FOR SEQ ID :1167:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 159 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:	
30	(III) DIGITION DIGITION DIGITION	
	GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAATG ACCTTTACGA	50
	AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG	100
35	GGACAGAATG AGAGAGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC	150
	ATCTGGAGA	159
40	(2) INFORMATION FOR SEQ ID :1168:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 211 base pairs	

593

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:	
10	CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG	50
10	CGATTGCCAC CGCTTCTCTC TAGTCTCACG AGGGGTTTCC CGCCTCGCAC	100
	CCCCACCTCT GGACTTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC	150
15	CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG	200
	GGGACCGATT C	211
20	(2) INFORMATION FOR SEQ ID :1169:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 211 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
25	(D) TOPOLOGY: linear	•
30	(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:	
	GGATTTCCGG TCCTGGCTTT CTGATATTTC TAAAATCGAC CTGGAATCAA	50
	CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC	100
35	CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT	, 150
	TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG	200
40	ATGAACACTT T	211
	(2) INFORMATION FOR SEO ID :1170:	

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(A) LENGTH: 266 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(i) SEQUENCE CHARACTERISTICS:

5	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1170:	•
10	GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA	50
	CAATGGAATG GGCGGAGGTC GAGGTNGACA AACCCTGAGT AATGTTGGGC	100
15	ACTTCCGCAC CGGAGCTGTT CTTACCTTTG ATAAAGTGGA TGTTATTGCT	150
	ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC	200
20	CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC	250
	GTTTGGGCTC AACGGC	266
	(2) INFORMATION FOR SEQ ID :1171:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 167 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1171:	
35	GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG	50
	CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG	100
40	GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC	150
70	TTTAATCCTT TAAAACT	167

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(2) INFORMATION FOR SEQ ID :1172:

5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 232 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1172:	
	AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC	50
15	TAATCCAGGA CAACCCACAA AAATTATAGC AACACAAAA CACACCGCTG	100
	ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT	150
20	TACTGAGGAT ACGCAACTCA TAAAACTCTA CTTAAAGCAA CAGGGCAGAC	200
20	GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC	232
	(2) INFORMATION FOR SEQ ID :1173:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
30	(b) TOPOLOGI: Timeat	
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1173:	
35	GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT	50
	CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC	93
40	(2) INFORMATION FOR SEQ ID :1174:	
40	(i) SEQUENCE CHARACTERISTICS:	

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
.5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:	
	GCCTTTTTTT ACCCGCCGGA AGCTACAGCT TTTGCCCCCC CAAAAAAACC	50
10	CCACCCTTTT ACCCACCGCG GACCCAAAAA CAGCAAAAAC CAAGGACCTC	100
	TCCCAACCC AACCCCTCCT TTTTGGCCCT TCCTTCCCCC CCTCCCAGCC	150
15	CACCCCAGA CACCTCAATC CCCCAAAAGG ATGCCCTAAA CCTCTCCTAA	200
	(2) INFORMATION FOR SEQ ID :1175:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 121 base pairs	
	(B) TYPE: nucleic acid	•
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
		-
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:	
30	GAGGATCCAA AAACCATGGC ATTCATCACG CCCAGCAGGT GTCCCAGCCA	50
	TGACTTACCA TAGCAAAACA CAACCACAC CTAACCTGCA TCGCCTAGCT	100
-	TACTGATGAT GATGTCCTGG T	121
35	(2) INFORMATION FOR SEQ ID :1176:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 26 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:	
	AACCAGACAC GCCGACCCGC TGAATC	26
5	(2) INFORMATION FOR SEQ ID :1177:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 178 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15 ·		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:	
	GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG	50
20	TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT	100
	CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT	150
25	TCAGGATGGA TTMAAGNAMG CAGAGAGG	178
	(2) INFORMATION FOR SEQ ID :1178:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 144 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:	
	GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA	50
40	AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTTGCCCGTG	100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAAGTTCAAG TCAA

200

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	(2) INFORMATION FOR SEQ ID :1179:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 233 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID :1179:	
	GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCG	50
15	AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG	100
	TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCACGCT TTGATTTACT	150
20	GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC	200
•	TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT	233
	(2) INFORMATION FOR SEQ ID :1180:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 225 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	•
30	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1180:	
35	CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC	50
	CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA	100
40	TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT	150

CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG

	AGGTAGACGG GACCAAGATC TGCTG	225
	(2) INFORMATION FOR SEQ ID :1181:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 293 base pairs	
	(B) TYPE: nucleic acid	. •
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:	
15	TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC	50
	GATGAATAAG CTTGATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA	100
20	TCNNNTTANT TTTTTGGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG	150
20	TTTAGAGTTT GGAAGCGGCN RNGCGTARMG NNACTCYACG CTCGCNNCTN	. 200
	TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRTNCMGTT GGMGGNNTCN	250
25	NUNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTGNGCTN GCT	293
	(2) INFORMATION FOR SEQ ID :1182:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 252 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:	
40	GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTTTTTTT	. 50
	GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA	100

600

	CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA	150
	GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC	200
5	TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT	250
	NG	252
	(2) INFORMATION FOR SEQ ID :1183:	
10	· · · · · · · · · · · · · · · · · · ·	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 202 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID :1183:	
20	ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG	50
	AAACTGTAGA TTCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG	100
25	AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT	150
	ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT	200
30	GT	202
30	(2) INFORMATION FOR SEQ ID :1184:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 43 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

	CAGATCCTCA GCTTTCGTGG TTCACAATTT CTTCAGTCTC TTA	43
	(2) INFORMATION FOR SEQ ID :1185:	٠
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 48 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:	
15	ACCGTCCTTC TGGTTCATCC TAGCAAAAT CTCACCATCT TCTATCAC	48
	(2) INFORMATION FOR SEQ ID :1186:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 104 base pairs	
-	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25		
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:	
30	ACATCATCCG AGTCCCCTCT ACAGTGTTCA TTGTGATCGT TGCATCCCCC	50
	TGGTTTGGAA ATAAAATATA AACTGCCCGG CAAGAGATAA AATTGTATTT	100
	TTTA	104
35	(2) INFORMATION FOR SEQ ID :1187:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 76 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

	(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:	
_	CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG	50
5	AGAATCCTAT TCAGTGCTCC CTTAGA	76
	(2) INFORMATION FOR SEQ ID :1188:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 42 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1188:	
20	AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA	42
	(2) INFORMATION FOR SEQ ID :1189:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 253 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1189:	
35	GGCGGACGTG CGCGCCTTGT CTTCGCGGCA CCTGGGCCTG AGGTGCGTGC	50
33	CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC	100
	GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC	150
40	GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC	200
	GTTTTAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC	250

•	AAT	253
	(2) INFORMATION FOR SEQ ID :1190:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 252 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
10	(D) TOPOLOGY: linear	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1190:	
15	GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG	50
		30
	TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA	100
20	CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT	150
20	GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC	200
		200
	AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT	250
25	TT	252
	(2) INFORMATION FOR SEQ ID :1191:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 178 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID :1191:	
40	GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA	50
	ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC	100

,	TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA	150
	CCCTTCCGGC TGCCCTTGTG TTGACTTG	178
5	(2) INFORMATION FOR SEQ ID :1192:	
	(i) SEQUENCE CHARACTERISTICS:	•
	(A) LENGTH: 156 base pairs	•
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID :1192:	
	GGATCGCCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT	50
	CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT	100
20		
-	GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG	150
	NGGGCA	156
25	(2) INFORMATION FOR SEQ ID :1193:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 99 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID :1193:	
	ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTTGT AATACAGACA	50
	TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA	99

	(2) INFORMATION FOR SEQ ID NO: 1194	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:	
	NNNNTCCTTC TCCTGCGACA GACA	24
15	(2) INFORMATION FOR SEQ ID NO: 1195	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:	
	TGTCTGTCGC AGGAGAAGGA	20
30	(2) INFORMATION FOR SEQ ID NO: 1196(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	·
•	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:	
40	AANNTCTCGG ACAGTGCTCC GAGAAC	26

	(2) INFORMATION FOR SEQ ID NO: 1197	•	
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 26 base pairs		
5	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
10			
_	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:		
	TTNNTCTCGG ACAGTGCTCC GAGAAC		26
15	(2) INFORMATION FOR SEQ ID NO: 1198		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 22 base pairs		
•	(B) TYPE: nucleic acid	•	
20	(C) STRANDEDNESS: single	•	
	(D) TOPOLOGY: linear		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:		
	GTTCTCGGAG CACTGTCCGA GA		22
	(2) INFORMATION FOR SEQ ID NO: 1199		
30			
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 23 base pairs	•	
•	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
35	(D) TOPOLOGY: linear		
	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:		
40	GTTCTCGGAG CACTGTCCGA GAG		23

	(2) INFORMATION FOR SEQ ID NO: 1200	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:	٠
	GTTCTCGGAG CACTGTCCGA GAC	23
15	(2) INFORMATION FOR SEQ ID NO: 1201	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:	
	CTGTCTGTCG CAGGAGAAGG AA	22
30	(2) INFORMATION FOR SEQ ID NO: 1202	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
•		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:	
	CTGTCTGTCG CAGGAGAAGG AG	22

	(2) INFORMATION FOR SEQ ID NO: 1203	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:	·
	AGCTCGGCTC GAGTCTG	17
15	(2) INFORMATION FOR SEQ ID NO: 1204	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:	
	GCGACAGACA GCAGACTCGA GCCG	24
30	(2) INFORMATION FOR SEQ ID NO: 1205 (i) SEQUENCE CHARACTERISTICS:	
·	(A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:	
	GATCCGGCTC GAGT	14

	(2) INFORMATION FOR SEQ ID NO: 1206	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:	
	CCGAGAACAC TCGAGCCG	18
15	(2) INFORMATION FOR SEQ ID NO: 1207	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid	÷
20	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:	
	GTAAAACGAC GGCCAGT	17
30	(2) INFORMATION FOR SEQ ID NO: 1208	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
-		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1208: CGAGGTCGAC GGTATCG	17
	•	

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	(2) INFORMATION FOR SEQ ID NO: 1209	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
•		
10	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:	
	CGAGGTCGAC GGTATCG	17
15	(2) INFORMATION FOR SEQ ID NO: 1210	
	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 56 base pairs	-
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:	
	TACGTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT	50
	TTTTTT	56
30	(2) INFORMATION FOR SEQ ID NO: 1211	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 11 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40		
••	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:	

611

	GCCWSCGCCG A	11
	(2) INFORMATION FOR SEQ ID NO: 1212	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 24 base pairs	
-	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	• ·	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:	
15	GGTGGCGACG ACTCCTGGAG CCCG	24
	(2) INFORMATION FOR SEQ ID NO: 1213	
•	· · · · · · · · · · · · · · · · · · ·	
20	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 24 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:	
	TTGACACCAG ACCAACTGGT AATG	24
30	Translation reconciled Anie	24
	In the above SEQUENCE LISTINGS, some sequences are preferred	l becau
25	thou fall into the enterem of account of the control of the contro	

In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40 85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291, 615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127, 1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

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- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- 10 (c) a sequence complementary to (a) or (b).
 - 2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
- 3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
 - 4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
 - 5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.

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- 6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
- 7. A nucleic acid sequence as claimed in claim 2 or claim 3 and encoding at least a portion of a biologically active polypeptide.
 - 8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.

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- 9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
- 40 10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

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protein and said fragment or sequence.

- 11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a gene.
- 12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.
- 13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.
 - 14. A vector as claimed in claim 13, wherein said vector control or regulatory sequence comprises a regulatable promoter.
 - 15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.
 - 16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.
 - 17. An antibody directed against a polypeptide obtainable by the performance of a process as defined in claim 16.
 - 18. An antibody as claimed in claim 17 and which is monoclonal.
- 19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.

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(57) Abstract

This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.

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INTERNATIONAL SEARCH REPORT

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). CLASSIFICATION OF SUBJ	JECT MATTER (if several classification of Classification (IPC) or to both National	symbols apply, indicate all) ⁶		
Int.Cl.5 C 07 K 15/28		12 N 15/62 C 12 P 2	1/08	
II. FIELDS SEARCHED				
	Minimum Docur	mentation Searched ⁷		
Classification System		Classification Symbols		
Int.Cl.5	C 12 N	C 12 Q C 07 K		
Documentation Searched other than Minimum Documentation to the Extent that such Documents are included in the Fields Searched ⁸				
III. DOCUMENTS CONSIDERI	ED TO BE RELEVANT®			
	ocument, 11 with indication, where appropr	riate, of the relevant passages 12	Relevant to Claim No.13	
pages DNA se genome	CE vol. 252, 21 June 19 1651 - 1656 ADAMS, M. equencing: expressed se project' e whole document	ET AL. 'Complementary	1-19	
OF USA 1943 - a unif cited	DINGS OF THE NATIONAL A vol. 88, March 1991, No. 1947 PATANJALI, S. ET orm-abundance (normalized in the application e whole document	WASHINGTON US pages AL. 'Construction of	1-19	
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"A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed IV. CERTIFICATION			ne application but y underlying the med invention considered to med invention ive step when the ther such docu- a person skilled	
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nternational Searching Authority EUROPEA	N PATENT OFFICE	Signature of Authorized Officer		
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Page 2 PCT/GB 93/01467

International Application No

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	STS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)	·
lategory "	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
	WINDLEY AND DESCRIPTION 3 10 10 11	
(NUCLEIC ACIDS RESEARCH vol. 18, no. 19, 11 October 1990, ARLINGTON, VIRGINIA US pages 5705 - 5711 KO, M.S.H. 'An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs' cited in the application see the whole document	1-19
	see the whole document	
,	NATURE vol. 355, 13 February 1992, LONDON GB pages 632 - 634 ADAMS, M. ET AL. 'Sequence identification of 2,375 human brain genes'	1-19
	see the whole document	
,	GENE vol. 81, 1989, AMSTERDAM NL pages 295 - 306 AKOWITZ, A. & MANUELIDIS, L. 'A novel cDNA/PCR strategy for efficient cloning of small amounts of undefined RNA' see the whole document	1-19
Υ .	WO,A,9302214 (MEDICAL RESEARCH COUNCIL) 4 February 1993 see the whole document	1-19
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Form PCT/ISA/210 (extra sheet) (January 1985)

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INTERNATIONAL SEARCH REPORT

Box 1	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This inte	mational search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
t. [_]	Claims Nos because they relate to subject matter not required to be searched by this Authority, namely:
2 -	Cianos Nos.:
	Chains Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3,	·
	Claims Nos., because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This Inte	mational Searching Authority found multiple inventions in this international application, as follows:
Set	e PCT/ISA/206 mailed on 29.11.93
ı. []	As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2 🗔	As all searchable claims could be searches without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3 . [_]	As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4: X	No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims. Nos.:
	1-19(all partially)
Remark	on Protest The additional search fees were accompanied by the applicant's protest.
	No protest accompanied the payment of additional search fees.
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